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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Nov 2 16:31:05 1998; MasPar time 19.22 Seconds 691.579 Million cell updates/sec

Tabular output not generated.

Title:

Description: erfect Score: equence:

>US-08-906-365-2 (1-530) from US08906365.pep 3904 1 MDIKNSPSSLNSPSSYNCSQ......ECSPAEDSKSKEGSQNPQSQ 530

Scoring table: PAM 150 Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 50.804; Variance 83.063; scale 0.612

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	50
3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Result No.
1698 1669 11663 11663 11603 11503 11	Score
43.5 42.6 42.6 42.6 42.6 42.6 41.1 41.1 117.1 117.1 115.6 115.7 115.7 115.3	Query Match
589 599 599 599 583 575 575 574 530 933 933 933 933 776 777 777 777 777 777 777 777 777 7	Length
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ESTR_HUMAN ESTR_HUMAN ESTR_MOUSE ESTR_RAT ESTR_ORFAL ESTR_ORYLA ESTR_ORYLA ESTR_ORYLA ESTR_SALAR ESTR_SALAR ESTR_SALAR ESTR_HUMAN PRGR_HUMAN PRGR_HUMAN PRGR_HUMAN PRGR_HUMAN GCR_SAGOE PRGR_CHICK GCR_MOUSE ESTR_BOVIN	ID
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0.00e+00 0.0	Pred. No.

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EARLY RESPONSE PROTEIN	MINERALOCORTICOID RECE	ORPHAN NUCLEAR RECEPTO	NERVE GROWTH FACTOR IN	RETINOIC ACID RECEPTOR	RETINOIC ACID RECEPTOR	RETINOIC ACID RECEPTOR	RETINOIC ACID RECEPTOR		MINERALOCORTICOID RECE	RETINOIC ACID RECEPTOR	RETINOIC ACID RECEPTOR	MINERALOCORTICOID RECE	RETINOIC ACID RECEPTOR	GLUCOCORTICOID RECEPTO	MINERALOCORTICOID RECE	ANDROGEN RECEPTOR.	ANDROGEN RECEPTOR (FRA	ANDROGEN RECEPTOR.	ANDROGEN RECEPTOR.	GLUCOCORTICOID RECEPTO	GLUCOCORTICOID RECEPTO
	3.67e-87			4.03e-88				1.60e-90			2.06e-93		2.24e-94	4.94e-97	2.17e-101	1.33e-102	7.59e-103	2.48e-103	1.42e-103	4.95e-105	4.95e-105

ALIGNMENTS

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th 43.5%; Score 1698; DB 1; Length 589;	179 244 C4-TIPE ZINC FINGERS (TWO). 179 199 C4-TYPE. 215 239 C4-TYPE. 245 304 HINGE. 305 589 STEROID-BINDING. 25 589 AA; 66746 MW; 85FF1F4A CRC32;	192; SU/192. 6536; 1GDC. ; T00264; ; T002	SUBCULTI: HOMOLIMEK. SUBCELLULAR LOCATION: NUCLEAR. SUBCELLULAR LOCATION: NUCLEAR. DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMA DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN. IN THE ABSENCE OF LICAND, STEROID HORMONE RECEPTORS ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS; HORMONE BINDIN GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM TRANSCRIPTIONAL START SITES. SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC NUCLEAR HORMONE RECEPTORS. (72102. C77102.	E FROM N.A. ; 86247578. ; 06247578. ; GREEN S., ARGOS P., KUMAR V., WALTER P., BORNERT J. p.; 5:891-897(1986). 5:891-897(1986). CITION: THE STEROID HORMONES AND THEIR RECEPTORS ARE I REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT LEFERATION AND DIFFERENTIATION IN TARGET TISSUES.	STANDARD; PRT; 589 AA. (REL. 06, CREATED) (REL. 35, LAST SEQUENCE UPDATE) EPTOR (ER) (ESTRADIOL RECEPTOR). S (CHICKEN). ETAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES;
		PROTEIN;	AL DOMAIN, MAIN. PHOUGHT BINDING R REAM OF	JM., INVOLVED IN CELLULAR	NEOGNATHAE;

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Matches :
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01-JUN-1994 (REL. 29, LA
01-NOV-1997 (REL. 35, LA
ESTROGEN RECEPTOR (ER) (
ESR1 OR ESR.
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P03372;
VARIANT ALA-447.
MEDLINE; 9225065
REESE J.C., KAT2
                                                                                                                                                                                                            MEDLINE; 91061891.
SCHWABE J.W.E., NEUHAUS D.,
NATURE 348:458-461(1990).
                                                                                                                                                                                                                                                                                                                                             GREEN S., WALTER P., CHAMBON P.;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 86146892.
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MEDLINE; 86122927.
GREENE G.L., GILMA P., WATERFIELD
SCIENCE 231:1150-1154(1986).
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                                                                                                          CHAMBON
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8:1981-1986(1989).
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246; Conservative
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C., KATZENELLENBOGEN
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LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDATE)

() (ESTRADIOL RECEPTOR).
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112; Mismatches 100;
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Best Local
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[6]
VARIANT CYS-160.
ANDERSEN T.I., WC
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ZN_FING
ZN_FING
DOMAIN
DOMAIN
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PROSTIE; ESO0031; NUCLEAR_RECEPTOR; 1.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
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EMBL; X03635; G31234; -.
EMBL; M12674; G182193; -.
PIR; A03244; ORHUE.
HSSP; P06536; 1GDC.
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VARIANT
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   428
                       477
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                                                                                                                                                                                                  238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

- IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS; HORMONE BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.

SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETTANCYON NUCLEAR HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                  SAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSC
  RVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPL
                                                     CVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIH
                                                                                      MISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGK
                                                                                                 MINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGK 416
                                                                                                                                 V-RELL--LD-ALSPEQLVLTLLEAEPPHVLISR--PSAPFTEASMMMSLTKLADKELVH
                                                                                                                                             IKRSKKNSLALSLTADQMVSALLDAEPP-ILYSEYDPTRPFSEASMMGLLTNLADRELVH
                                                                                                                                                                           QACRIRKCYEVGMVKCGSRRERCGYRLVR--RQRSADE-QLHCAGKA-KRSGG--HAP-R
                                                                                                                                                                                                QACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGEGRGEVGSAGDMRAANLWPSPLM
                                                                                                                                                                                                                        SKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSC
                                           CVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA-DSSRKLA
                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T00261; -
                                                                                                                                                                                                                                                                                                            595
                                                                                                                                                                                                                                                                                                                                                                                      185
185
221
251
311
160
400
                                                                                                                                                                                                                                                                                                                                           447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEROID-BINDING; POLYMORPHISM.

1 184 MODULATING.
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                            ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267:9868-9873(1992).
                                                                                                                                                                                                                                                                          43.4%;
                                                                                                                                                                                                                                                                                                                                                                                      184
250
205
245
310
310
160
400
                                                                                                                                                                                                                                                                                                                                           447
                                                                                                                                                                                                                                                                                                            66216
                                                                                                                                                                                                                                                                                                            Œ;
                                                                                                                                                                                                                                                                 98;
                                                                                                                                                                                                                                                                           Score 1693; DB 1;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                 DECREASES ITS AFFINITY FOR ESTRADIOL A 25 DEGREES CELSIUS, BUT NOT AT 4 DEGRE CELSIUS)
                                                                                                                                                                                                                                                                                                                                                                                                                              C4-TYPE ZINC
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                   STEROID-BINDING.
G -> C.
G -> V (DESTABILIZES
                                                                                                                                                                                                                                                                                                                                C -> A (LOSS OF HORMONE BINDING AND TEMPERATURE-SENSITIVE LOSS:
                                                                                                                                                                                                                                                                                                                      BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                      HINGE.
                                                                                                                                                                                        <del>-</del>
                                                                                                                                                                                                                                                                                                            D6945BB9
                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                            CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FINGERS
                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TWO).
                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN;
                                                                                                                                                                                                                                                                                                                                 G CAPACITY
                                                                                                                                                                                                                                                                                                                                                                 DEGREES
                                                                                                                                                                                                                                                                 Gaps
                                                                  476
                                                                                                                                                       356
                      536
                                                                                                                                 308
                                                                                                                                                                             254
                                                                                                                                                                                                 297
                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                            ΑŦ
   487
                                            427
                                                                                      368
                                                                                                                                                                                                                                            237
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YDLLLEMLDAHRLHA-PTSRGGASVEETDQSHLATAGSTSSHS

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                                                                                                                                                                                             Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:
PROSITE;
                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               + + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991 (REL.
01-FEB-1991 (REL.
01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESTR_MOUSE P19785;
                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=UTERUS;
MEDLINE; 91042558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR) ESR1 OR EST OR ESTRA.
                                                                                                                                                                                                                                                                                                                              ZINC-FINGER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUTHERIA;
243
                        287
                                                187
                                                                     227
                                                                                               131
                                                                                                                    167
                                                                                                                                                                    108
                                                                                                                                              73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE 1 THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES TRANSCRIPTIONAL START SITES.
SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMA:
A DNA-BINDING DOMAIN AND A C-TERMINAL STERCID-BINDING DOMAIN.
IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS ARE THOUGHT
TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS; HORMONE BINDING
GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBURIT: HOMODIMER.
SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEAR HORMONE RECEPTORS.; M38651; G193180; -.
                                                                                                                                                                                                                                                                                                                                                                                                      A40061
                                                                                                                                                                                                                                                                                                                                        MGI:109348; ESTRA.
ITE; PS00031; NUCLEAR_RECEPTOR;
PTOR; TRANSCRIPTION REGULATION;
                                            ERLSSSNEKGNMIMESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCP 226
                                                                                                                                                                  SPSPLMLLHPPPQLSPFLHPHGQQVPYYLENEPSAY-AVRDTGPPAFYRSNSDNRRQNGR 166
GKAKRSGG--HAPRV-RELLLD--ALS--PEQLVLTLLEAEPPHVLIS-RPSAPFTEASM
                                                                                            NR-CASPVTGP---GSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICP
                                                                                                                                           TTSPNVLWPTPGHLSP-LVVHRQLSHLYAEPQKSPWCEARSLEHTLPVNRETLKRKVSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENDOCRINOL. 1:735-744(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YDLLLEMLNAHVLRGCKSSITGSECSPAEDSK-SKEGSQNPQS 529
                     SGDMRAANLWPSPLVIKHTKKNSPALSLTADQMVSALLDAEPPMIYSEYDPSRPFSEASM
                                                                                                                                                                                                                                                                                                                                                                                            P06536;
                                                                                                                                                                                                                                                                                                                                                                                                      M38651; G19318
140061; A40061.
                                                                                                                                                                                             246;
                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RODENTIA.
                                                                                                                                                                                                                                             599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAZOA;
                                                                                                                                                                                                                                                                    189
189
225
255
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                               STEROID-BINDING
                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17, CREATED)
17, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                        42.8%;
51.7%;
                                                                                                                                                                                                                                                                  188
254
209
599
                                                                                                                                                                                                                                             66955 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                             106;
                                                                                                                                                                                                                                                                 MODULATING.
C4-TYPE ZINC FINGERS (
C4-TYPE.
C4-TYPE.
C4-TYPE.
STEROID-BINDING.
                                                                                                                                                                                                        Score 1669; DB 1;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                        POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                            6ED9EADB CRC32;
                                                                                                                                                                                             Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAM J.,
                                                                                                                                                                                                                                                                                                                                         DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A MODULATING N-TERMINAL DOMAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                          STEROID/THYROID/RETINOIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARKER M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                 Length 599;
                                                                                                                                                                                                                                                                                                                                           NUCLEAR PROTEIN;
                                                                                                                                                                                           Indels 20;
                                                                                                                                                                                                                                                                                                       (OWI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HORMONE BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UPSTREAM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELLULAR
                                                                                                                                                                                          Gaps
                     346
                                                                                                                                           130
                                             242
                                                                    286
                                                                                            186
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RESULTS OF THE PROPERTY OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBMITTED (JUN-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE J
THE REGULATION OF BURKRYOTIC GENE EXPRESSION AND AFFECT
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                   EMBL; Y00102; G56111; -.
EMBL; X61098; G56121; -.
EMBL; S07379; S07379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 87174780. KOIKE S., SAKAI M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1988 (REL.
01-JAN-1988 (REL.
01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOIKE S., SAKAI M. NUCLEIC ACIDS RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P06211;
                                                                                                                                                         DOMAIN
                                                                                                                                                                              RECEPTOR; TR
ZINC-FINGER;
                                                                                                                                                                                                                                              TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAGGI A.M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY; TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MURAMATSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RATTUS NORVEGICUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESTROGEN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESTR_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295
                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS; HORMONE BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.

SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
                                                                                                                                                                                                                                                                                                                                                      NUCLEAR HORMONE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGM
::| ::|::|::|::|::|::|:|:|:||
TATQDA-DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR ESR OR ESTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHLLNMKCKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSQNPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EHLYNMKCKNVVPLYDLLLEMLDAHRLHAPASRMGVPPEEPSQTQLATTSSTSAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGLLTNLADRELVHMINWAKRVPGFGDLNLHDQVHLLECAWLEILMIGLVWRSMEHPGKL
                                                                                                                                                                                                                                                                   P06536; 1GDC
                                                                                                                                                                                                PS00031; NUCLEAR_RECEPTOR; TRANSCRIPTION REGULATION;
                                                                                                                                                                                                                                              T00258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MAR-1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAZOA;
                         190
190
226
256
488
                                                                                                                                                                              STEROID-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06, CREATED)
06, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
(ER) (ESTRADIOL RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15:2499-2513(1987)
488
67030
                                           189
255
210
250
600
71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GENBANK/DDBJ
  WW.
                MODULATING.
C4-TYPE ZINC FIN
C4-TYPE.
C4-TYPE.
STEROID-BINDING.
POLY-ALA.
N-> T (IN REF.
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-> T (IN :
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Local Match

Similarity

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SERVICE SERV
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01-NOV-1997 (REL. 3
01-NOV-1997 (REL. 3
01-NOV-1997 (REL. 3
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ESTR_PIG
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ESR1 OR ESR.
SUS SCROFA (PIG).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA;
EUTHERIA; ARTIODACT
                                                NUCLEAR HORMONE RECEPTORS.
EMBL; 237167; G587555; -.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
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                                                                                                                    SUBUNIT: HOMODIMER.

SUBCELLULAR LOCATION: NUCLEAR.

SUBCELLULAR LOCATION: NUCLEAR.

SUBCELLULAR LOCATION: NUCLEAR.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOI DOMAIN.

A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS ARE THOUGH TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS; HORMONE BIND GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM TRANSCRIPTIONAL START SITES.

TRANSCRIPTIONAL START SITES.

SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
                                                                                                                                                                                                                                                                                                                                                             KENKAMP D., JUNGBLUT P.W., THOLE H.H.;
CELL, ENDOCRINOL. 104:163-172(1994).
FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE 1
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGLLTNLADRELVHMINWAKRVPGFGDLNLHDQVHLLECAWLEILMIGLVWRSMEHPGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A--KRSGG--HAPRV-RELLLD--ALS--PEQLVLTLLEAEPPHVLIS-RPSAPFTEASM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGDMRAANLWPSPLVIKHTKKNSPALSLTADQMVSALLDAEPPLIYSEYDPSRPFSEASM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NR-CASPVTGP---GSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHLYNMKCKNVVPLYDLLLEMLDAHRLHAPASRMGVPPEEPSQSQLTTTSSTSAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSTLKSLEEKDHIHRVLDKINDTLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHLLNMKCKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSQNPQS
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     TRANSCRIPTION REGULATION; ER; STEROID-BINDING.
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larity 51.1%;
Conservative
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LAST ANNOTATION UPDATE)
(ESTRADIOL RECEPTOR).
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Pred. No. 0.00e+00;
L10; Mismatches 103;
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                           DNA-BINDING;
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                                                                                                                                                                       PONENTS; HORMONE BINDING HORMONE-RECEPTOR A SEQUENCES UPSTREAM OF
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SEQUENCE
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P50240;
01-OCT-1996
01-NOV-1997
01-NOV-1997
                                                                                                                                                                            ESTROGEN
ESR.
TAN N., LAM T., DING J.;
DNA SEQ. 5:359-370(1995).

IN SEQ. 5:359-370(1995).

IF FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE I
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

IS SUBUNIT: HOMODIMER (BY SIMILARITY).

IS SUBCELLULAR LOCATION: NUCLEAR.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMIN
                                                                   SEQUENCE OF 270-583
TISSUE=BLOOD;
MEDLINE; 96272302.
                                                                                                                                                          OREOCHROMIS AUREUS. EUKARYOTA; METAZOA;
                                                                                                        MEDLINE; 97120581.
TAN N.S., LAM T.J., DII
MOL. CELL. ENDOCRINOL.
                                                                                                                                 SEQUENCE
                                                                                                                                                    OSTEICHTHYES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 SPSPLVLLHPPPQLSPFLHPHGQQVPYYLENEPSGY-AVREAGPPAFYRPNSDNRRQGGR 162
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||| ||||||||||:|| ||::
EHLLNMKCKNVVPVYDLLLEMLNAHVLRG
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(REL.
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                                                                                                                                  N.A.
                                                                                                                                                   TAZOA; CHORDATA;
ACTINOPTERYGII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                    . 34, CREATED)
. 35, LAST SEQUENCE UPI
. 35, LAST ANNOTATION C
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DL. 123:149-161(1996).
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                                                                                        N.A.
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C4-TYPE ZINC FINGERS (TWO).
C4-TYPE.
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STEROID-BINDING.
W; E50DF7AC CRC32;
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Pred.
97; M
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PERCIFORMES
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No. 0.00e+00;
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                                                                                                                                                             PISCES;
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  N-TERMINAL
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T CELLULAR
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P50241;
01-OCT-1996
01-OCT-1996
01-NOV-1997
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X93559; E256017; JOINED.
X93569; E256017; JOINED.
X93560; E256017; JOINED.
L; 246665; E256017; JOINED.
L; 246666; E256017; JOINED.
L; 246668; E256017; JOINED.
L; 246669; E256017; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A DNA-BINDING
SIMILARITY: TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEAR HORMONE
                                                                                     QQQSRRQAQLLLLLSHIRHMSNKGMEHLYSMKCKNKVPLYDLLLEMLDAHRIHRPVKPS
                                                                                                                          LKLKPEEFVCLKAIILLNSGAFSFCTGTMEPLHDSVAVQHMLDTITDALIFHISHFGCSA 451
                                                                                                                                                     LLEAEPPHYLISRPS-A-PFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFDQVR
                                                                                                                                                                                                     LQGAEPP-ILCSRQKMSRPYTEYTIMTLLTSMADKELVHMITWAKKLPGFLQLSLHDQVL
                                                                                                                                                                                                                                                                                                                                                               YSAPLDAHG-PLSDGSLQS-LGSGPTSPLVFVPSSPRLSFFM-HPP-SHHYLETTSTP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 246669; E256017;
; Z46665; E212276;
; Z46666; E212276;
; Z46666; E212276;
                                                                                                                LKLOHKEYLCVKAMILLNSSMYPLVTATQDA-DSSKKLAHLLNAVTDALVWVIAKSGISS
                                                                                                                                                                                                                                                                        EGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGY
                                                                                                                                                                                                                                                                                   EGCKAFFKRSIQGHNDYMCPATNQCTIDKNRKKSCQACRLRKCYEVGMMKGGMRKDR-G-
                                                                                                                                                                                                                                                                                                              EARSLEHTLPVNRETLKRK-V-SGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSC
                                                                                                                                                                                                                                                                                                                                  VYRSSHQPVPREDQCGTRDEAYSVGELGAGAGGFEITKNTRFCAVCSDYASGYHYGVWSC
                                                                                                                                                                                                                                                                                                                                                     YSPAVMNYSIPSNYTNLEGGPGRQTTSPNYLWPTPGHLSPLVVHRQLSHLYAEPQKSPWC
                                                                            QQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAH-VLRGCKSS
                                                                                                                                                                                                                                   RLVRRQR--SAD-E--Q-L--H--CA--G-K-AKRSGGHA-PRVRELLLDALSPEQLVLT
                                                                                                                                                                                                                                                     RVLRREKHGPAQRQTSQNLPTHKASPQDGRKRAMSSSSTSGPGGRSSL-NNMPPDQVLLL
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Z46669; E212276;
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(REL.
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                                       STANDARD;
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35,
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O OTHER MEMBERS
                                                                                                                                                                                                                                                                                                                                                                                                    41.18;
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CREATED)
LAST SEQUENCE UI
LAST ANNOTATION
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Pred. No. 0.00e+00;
90; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                         C4-TYPE ZINC FINC
C4-TYPE.
C4-TYPE.
STEROID-BINDING (
POLY-LEU.
POLY-LEU.
POLY-GIY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.
DNA-BINDING; NUCLEAR
            UPDATE )
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ZINC FINGERS (TWO)
                                      575
 UPDATE)
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SEQUENCE
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-:- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ATTHE REGULATION OF EURARYOTIC GENE EXPRESSION AND AFF
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORYZIAS LATIPES (MEDAKA FISH).
EUKARYOTA; METAZOA; CHORDATA;
OSTEICHTHYES; ACTINOPTERYGII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR). ESR. ORYZIAS LATIPES (MEDAKA FISH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC-FINGER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-1- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC NUCLEAR HORMONE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OKADA H
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  445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                        PAMTEYSPAVMNYSIPSNVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQ 103
GVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRR
                                                                                                                                                                                                                         GVWSCEGCKAFFKRSIQGHNDYMCPAINQCTIDRNRRKSCQACRLRKCYEVGMMKGGVRK
                                          RFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA-DSSRKLAHLLNAVTDALVWVIAKS
                                                    RFRVLKLKPEEFVCLKAIILLNSGAFSFCTGTMEPLHNSAAVQSMLDTITDALIHYISQS 452
                                                                                    DQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTS
                                                                                              DQVLLLESSWLEVLMIGLIWRSIHCPGKLIFAQDLILDRNEGDCVEGMTEIFDMLLATAS
                                                                                                                             LVLTLLEAEPPHVLISRPS-A-PFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLF
                                                                                                                                                                                                                                                         KSPWCEARSLEHTLPVNRETLKRKVS-GNRCASPVTGPGSK-RDAHFCAVCSDYASGYHY
                                                                                                                                                                                                                                                                              STPVYRSSHQGASREDQCGSREDTCSLGELGAGAGAGGFEMAKDTRFCAVCSDYASGYHY 153
                                                                                                                                                                                                                                                                                                                       SSTGYYSAPLETNGPPSE-GSLQS-LGSGPTSPLVFVPSSPRLSPFM-HPP-SHHYLETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D28954; G602326;
                                                                                                                                                                                                                                                                                                                                              h 40.8%;
Similarity 52.8%;
252; Conservative
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141
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Pred. No. 0.00e+00;
93; Mismatches 108
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C4-TYPE.
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D9FE40D0
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DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC
                                                                                                                                                                                                                                                                                                                                                                                        CRC32;
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                                                                                                                                                                                                                                                                                                                                              108;
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                                                                                                                                                                                                                                                                                                                                              Indels
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 501
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01-APR-1990 (REL.
01-APR-1993 (REL.
01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                  ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SALMO IRIDEUS (RAINBOW TROUT)
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESTROGEN
                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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 441
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; A40070; A40070.
P; P06536; IGDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEL F., LE GUELLEC C., VALLLANT C., LE ROUX M.G., VALOTA E ENDOCRINOL. 3:44-51(1989).
FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO OTHER MEMBERS NUCLEAR HORMONE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM TRANSCRIPTIONAL START SITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS; HORMONE BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN. A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS ARE THOUGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT:
                                                                                                                                                                                                                                   ETRYCAVCSDFASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTMDRNRRKSCQAC::::|||||||:||:||||||||
                                                                                                                                     SINGGGGWRGPRITMPPEQVLFILQGQTP-ALCSRQKVARPYTEVTMMTLLTSMADKELV 320
                                                                                                                                                                                    RLRKCYEVGMVKGGLRKDRGG-RVLRKDKRYCGPAGDREKPTVTWSTGQRPQDGGRNSSS
                                                                                                                                                                                                                        DAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQAC
                       KCVEGILEIFDMLLATISRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA-DSSRKL
                                                DCVEGMAEIFDMLLATVSRFGMLKLKPEEFVCLKAIILLNPGAFSFCSNSVESLHNSSAV
                                                                                   HMIAWAKKYPGFQELSLHDQVQLLESSWLEVLMIGLIWRSIHCPGKLIFAQDLILDRSEG
ESMLDNITDALIHHISHSGASVQQQPRRQAQLLLLLSHIRHMSNKGMEHLYSIKCKNKVP
                                                                        HMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEG
                                                                                                                         RVREL--LLDA-LS-PEQLVLTLLEAEPPHVLISRPS-A-PFTEASMMMSLTKLADKELV
                                                                                                                                                                       RLRKCYEVGMVKCGSRRERCGYRLVRRQ-R---SA-D-EQLHCA-GKAKRS--GGH--AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 91006824.
F., LE GAC F., L
LL. ENDOCRINOL.
                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       PS00031; NUCLEAR_RECEPTOR; 1.
; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR
                                                                                                                                                                                                                                                                                                                                  147
147
183
213
                                                                                                                                                                                                                                                                                                                                                                                               STEROID-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMODIMER.
                                                                                                                                                                                                                                                                        Conservative
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167
207
574
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56.38;
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                                                                                                                                                                                                                                                                                                                         62872 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
                                                                                                                                                                                                                                                                      Score 1516; DB 1;
Pred. No. 0.00e+00;
78; Mismatches 75
                                                                                                                                                                                                                                                                                                                                  C4-TYPE ZINC FING
C4-TYPE.
C4-TYPE.
STEROID-BINDING
                                                                                                                                                                                                                                                                                                                                                                                  MODULATING
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                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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P50242;
01-OCT-1996
01-OCT-1996
01-NOV-1997
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DOMAIN
DNA_BIND
ZN_FING
ZN_FING
DOMAIN
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SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSTEICHTHYES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X89959; G929902; -.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
RECEPTOR; TRANSCRIPTION REGULATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC-FINGER;
                                                                                                                                                                                                                                                                                                                                                                                                                          101 ETRYCAVCSDFASGYHYGFWSCEGCKAFFKRSIQGHNDYMCPATNQCTMDRNRRKSCQAC
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_SALSA
                                                                                                                                                                                                                                                                                                                                             RLRKCYEVGMVKGGLRKDRGG-RVLRKDKRYCGPAGDREKPYGDLEHRTAPPQDGGRNSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVP
                                                                                                                                                                                 LVHMIAWAKKVPGFQELSLHDQVQLLESSWLEVLMIGLIWRSIHCPGKLIFAQDLILDRS
                                                                                                                                                                                                                                       VRELL----L-DA-LS-PEQLVLTLLEAEPPHYLISRPS-A-PFTEASMMMSLTKLADKE
                                                                                                                                                                                                                                                                                                                    DAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQAC
                                                                                                    EGDCVEGMAEIFDMLLATVSRFRMLKLKPEEFVCLKAIILLNSGAFSFCSNSVESLHNSS
                                                                                                                                                            LVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRD
                                                                                                                                                                                                                                                                KLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNV
                                   AVESMLDNITDALIHHISHSGASVQQQPRRQVQLLLLLSHIRHMSNKGMEHLYSIKCKNK
                                                                             EGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA-DSSR
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. 34, LAST SEQUENCE UPD
. 35, LAST ANNOTATION UPD
R (ER) (ESTRADIOL RECENTABLE)
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C4-TYPE ZINC FINGERS (
C4-TYPE.
C4-TYPE.
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SALMONIFORMES
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No. 0.00e+00;
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Best Local :
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P11475;

01-0CT-1989 (REL. 1

01-0CT-1989 (REL. 1

01-0CT-1994 (REL. 3

STEROID HORMONE REC
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    ERR1.
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HFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRL
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                                                                                                                                                                                                                                                                                                              QVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSR
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TRANSCRIPTION REGULATION; DNA-BINDING;
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larity 39.5%;
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12, LAST SEQUENCE UPDATE)
30, LAST ANNOTATION UPDATE)
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Pred. No. 9.34e-162;
84; Mismatches 108;
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C4-TYPE.
C4-TYPE.
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ZN_FING
SEQUENCE
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-!- SUBCELLULAR LOCATION: NUCLEAR
-!- SIMILARITY: TO OTHER MEMBERS C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA;
[1]
                 SEQUENCE FROM N.A.

STRALH-ROMANOV; TISSUE-UTERUS;

STRALH-ROMANOV; TISSUE-UTERUS;

MADJGOU T., TIEFOCHE C., LE GAL F., PELLETIER J., THIEULANT

SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

-i- FUNCTION: THE STEROLD HORMONES AND THEIR RECEPTORS ARE I

THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT

PROLLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

-i- SÜBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                  OVIS ARIES
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01-NOV-1997
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01-NOV-1997
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                           PROGESTERONE
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                                                                                                                                                                                                         EUTHERIA;
                                                                                                                                                                                                                               EUKARYOTA;
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R; A29345; A29345.
SP; P06536; 1GDC.
SSITE; PS00031; NUCLEAR
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ARTIODACTYLA.
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7 (REL. 35, LAST SEQU
7 (REL. 35, LAST ANNO
NE RECEPTOR (PR) (FRA
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Matches
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01-DEC-1992 (REL. 24, C
01-DEC-1992 (REL. 24, I
01-NOV-1997 (REL. 35, I
PROCESTERONE RECEPTOR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
ZN_FING
ZN_FING
DOMAIN
                             HAGIHARÁ K., WÜ-PENG X.S., FUNABASHI T., KATO J., PFAFF D.W.;
BIOCHEM. BIOPHYS. RES. COMMUN. 205:1093-1101(1994).

-I- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

-I- SUBCELLULAR LOCATION: NUCLEAR.
-I- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-I- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
                                                                                                                                                                                      MEDLINE;
SCHOTT D.
EMBL;
                                                                                                                                         SEQUENCE OF 1-9
STRAIN=129/SV;
                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 91299759.
                                                                                                                                                                                                                                                    PGR
MUS
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                                                                                                                                                                          BIOCHEMISTRY
                                                                                                                                                                                                                                        EUKARYOTA;
                                                                                                                                                                                                                                                                                                                              PRGR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                MEDLINE;
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MUSCULUS (MOUSE).
MUSCULUS (MOUSE).
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SIMILARITY: TO
                      NUCLEAR HORMONE RECEPTORS
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                                                                                                                                                                                                                                                                                                                                                                         LATTSRFRELKLOHKEYLCVKAMILLNS-SMYPLVTATQ-DADSSRKLAHLLNAV
                                                                                                                                                                                                                                                                                                                                                                                                                                 HIDDQITLIQYSWMSLMVFGLGWRSYKHGSGQMLYFAPDLILNEQRMK-ESSFYSLCLTM
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                                                                                                                                                                                                                                                                                                                                                                                             WQIPQEFVKLQVSQEEFLCMKVLLLLNTIPLEGLRSQNQFEEMRSSYITQLIKAI
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 M68915;
U12644;
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102; Conser
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larity 34.6%;
Conservative
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30:7014-7020
G200472;
G639917;
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24, LAST SEQUENCE 35, LAST ANNO
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78
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LAST
(PR).
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ANNOTATION UPDATE)
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Pred. No. 5.2
82; Mismatch
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C4-TYPE ZINC FINC
C4-TYPE.
C4-TYPE.
STEROID-BINDING.
                                                                                                                                                                                                                                        VERTEBRATA;
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DNA-BINDING; NUCLEAR
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.25e-130;
.ches 98;
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RESULTATION OF THE PROPERTY OF
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Best Local S
Matches 12
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 87184565.

MISRAHI M., ATGER M., D'AURIOL L., LOOSFELT H., MERLEL ...

FRIDLANSKY F., GUIOCHON-MANTEL A., GALLBERT F., MILGROM E.;

BIOCHEM. BIOPHYS. RES. COMMUN. 143:740-748(1987).

-!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN

THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR

THE REGULATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988
01-AUG-1990
01-OCT-1996
                                                                                                                                                                                                                                                                             MEDLINE;
KASTNER I
CHAMBON I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                          EMBO J.
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 90228361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROGESTERONE
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HSSP; P06536; 1GDC.
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557
593
671
184
923
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(REL. 15, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                TURCOTTE
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112; ;
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Pred. No. 1.
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C4-TYPE.
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NUCLEAR LOCALIZATION
: EEDFF41A CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                   VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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DNA-BINDING;
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                                                                                                                                                                                                                                                                                                                                                                                                     TETRAPODA;
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                                                                                                                                                                                                                                                                                                                                                                                                     MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   923;
                                                                                                                                                                                                                                                                                                  GRONEMEYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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Best Local Similarity
Matches 110; Conser
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EMBL; M15716; G189935; -.
PIR; A03245; ORHUP.
PIR; S09971; S09971.
HSSP; P06536; IGDC.
                                       PRGR_RABIT
P06186;
01-JAN-1988
01-JAN-1988
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                      PROGESTERONE
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RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC-FINGER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC;
                                                                                                                                                                                                       440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: NUCLEAR.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DANA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

ALTERNATIVE PRODUCTS: THERE ARE TWO FORMS OF THE PROGESTERONE
RECEPTOR: FORM A (THAT STARTS WITH MET-1) AND FORM B (THAT STARTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEAR HORMONE RECEPTORS
                                                                                                                                                                                                                                           LRQKGVVSSSQRFYQLTKLLDNLHDLVKQ 886
                                                                                                                                                                                                                                                                                                     WQIPQEFVKLQVSQEEFLCMKVLLLLNTIPLEGLRSQTQ-FEEMRS-SYI-RELIKAIG-
                                                                                                                                                                                                                                                                                                                                                             SLFDQVRLLESCWMEVLMMGLMWRSIDH-PGKLI-FAPDLVLDRDEGKCVEGILEIFDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ICLICGDEASGCHYGVLTCGSCKVFFKRAMEGQHNYLCAGRNDCIVDKIRRKNCPACRLR
                                                                                                                                                                                                 VIAKSGISSQQQSMRLANLL-MLLSHVRH
                                                                                                                                                                                                                                                                                                                                                                                  SPEQLVLTLLEAEPPHVLISRPSA-PFTEASMMSLTKLADKELVHMISWAKKIPGFVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCYEVGMVKCGSRRERCGYRLVRRQRSADE-QL-HCAGKAKRSGGHAPRVR-ELLLDA-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KCCQAGMVL-GGRKFK-KFNKVRVVRALDAVALPQPLGVPNESQALSQRFTFSPGQDIQL
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                                                                                                                                                                                                                                                                                  LATTSRFRELKLOHKEYLCVKAMILLNS-SMYPLVTATQDADSSRKLAHLLNAVTDALVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IP-PLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNL
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                      (REL. 06,
(REL. 06,
(REL. 34,
E RECEPTOR
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567
603
681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä
                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO OTHER MEMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       660
99042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.1%;
33.4%;
                                       CREATED)
LAST SEQUENCE UI
LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 666; DB 1; L. Pred. No. 8.35e-127; 89; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISSING (IN FORM B
S -> G (IN REF. 2)
C -> V (IN REF. 2)
T -> S (IN REF. 2)
L -> V (IN REF. 2)
OD1124EB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C4-TYPE ZINC FINGERS (C4-TYPE. C4-TYPE. STEROID-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY CK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MODULATING,
                                                                                                                      PRT;
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                                                              UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Best Local
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ZN_FING
ZN_FING
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A25923; A25923.
HSSP; P06536; 1GDC
TRANSER?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE: 87067449.

LOOSFELT H., ATGER M., MISRAHI M., GUIOCHON-MANTEL A., MERIE LOGSFELT H., BENAROUS R., MILGROM E.,

PROC. NATL. ACAD. SCI. U.S.A. 83:9045-9049(1986).

-!- FUNCTION: THE STEROID HORNONES AND THEIR RECEPTORS ARE I THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

-!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; LAGOMORPHA.
[1]
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC-FINGER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T00697; -.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   148
                                                                                                                                                                                                                                                                             567 ICLICGDEASGCHYGVLTCGSCKVFFKRAMEGQHNYLCAGRNDCIVDKIRRKNCPACRLR 626
 443
                                                                                                                                                                                                                                         627
                                                    383
                                                                                                       325
                                                                                                                               742
                                                                                                                                                           266
                                                                                                                                                                                                               208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: TO OTHER MEMBERS OF THE NUCLEAR HORMONE RECEPTORS.
                                                                                                                    DDQITLIQYSWMSLMVFGLGWRSYKHVSGQMLYFAPDLILNEQRMK-ESSFYSLCLTMWQ
                                                                                                                                                                                                                          KCCQAGMVL-GGRKFK-KFNKVRVMRALDAVALPQPVGIPNESQ-RITFSPSQEIQ-LIP 682
                                                                                                                                                                                                                                                                  FCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLR
KSGISSQQQSMRLANLL-MLLSHVRH
                        KGVVSSSQRFYQLTKLLDNLHDLVKQ
                                                  TTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIA
                                                                           IPQEFVKLQVSQEEFLCMKVLLLLNT-I-PLEGLRSQSQFEEMRSSYIRELIKAIG-LRQ
                                                                                                  FDQVRLLESCWMEVLMMGLMWRSIDH-PGKLI-FAPDLVLDRDEGKCVEGILEIFDMLLA
                                                                                                                                                        EQLVLTLLEAEPPHVLISRPSA-PFTEASMMSLTKLADKELVHMISWAKKIPGFVELSL
                                                                                                                                                                          -PLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNLHI
                                                                                                                                                                                                              KCYEVGMVKCGSRRERCGYRLVRRQRSADE-QL-HCAGKAKRSGGHAPRVRELLLDALSP
                                                                                                                                                                                                                                                                                                                     106;
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSCRIPTION REGULATION;
                                                                                                                                                                                                                                                                                                                                                                       568
568
604
678
184
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEROID-BINDING
                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                       633
588
628
930
188
98666 MW;
                                                                                                                                                                                                                                                                                                                                 17.0%;
                                                                                                                                                                                                                                                                                                                                                                      C4-TYPE ZINC FINGERS (
C4-TYPE.
C4-TYPE.
STEROID-BINDING.
NUCLEAR LOCALIZATION S
W; EE133E86 CRC32;
                                                                                                                                                                                                                                                                                                                     Pred.
91; N
                                                                                                                                                                                                                                                                                                                                 Score 662; DB 1; L
Pred. No. 8.05e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                        MODULATING, I
                        883
                                                                                                                                                                                                                                                                                                                     Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO-RICH.
                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR
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                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                               930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MERIEL
                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN;
                                                                                                                                                                                                                                                                                                                     15;
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Search completed: Mon Nov 2 16:32:02 1998 Job time: 57 secs.

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Nov 3 04:56:49 1998; MasPar time 74.31 Seconds 1058.292 Million cell updates/sec

Tabular output not generated.

Title: >US-08-906-365-1 (1-1686) from US08906365.seq 1686

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 cagccattatacttgcccac......agaacccacagtctcagtga 1686 gtcggtaatatgaacgggtg......tcttgggtgtcagagtcact

Scoring table: TABLE default Gap 6

Nmatch STD: Dbase 0; Query 0

Searched: 88822 seqs, 23323279 bases x

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 9.055; Variance 4.480; scale 2.021

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score 197	Query Match	Length 4963	B	08	ion 16,	ed. No
c 2 3 2	197 71		4963 3460		US-08-260- US-08-312-	1, 2, 4	.47e-1
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15	42	2.5	2940	ω ,	5171671-1	Patent No. 5171671.	8.39e-1 8.39e-1
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17	ω	2.3	1662	N	PCT-US91-0	-	4.95e-1
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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Applicatio	92, Applicati	Applicati															Applicati	Applicatio						
4.05e-02	4.05e-02	4.05e-02	4.05e-02	4.05e-02	2.73e-03	2.73e-03	2.73e-03	2.73e-03	2.73e-03	2.73e-03	1.06e-02	1.06e-02	1.06e-02	1.06e-02	1.06e-02	1.67e-04	1.67e-04	1.67e-04	1.67e-04	4.01e-05	9.42e-06	9.42e-06	1.10e-07	1.10e-07
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ALIGNMENTS

3888888	88888888888	888888888888	RESULT AC AC AC CC
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 4963 base pairs TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: both SEQUENCE 4963 BP; 1259 A; 1300 C; 1278 G; 1126 T; 0 OTHER.	ICATION DATA: N NUMBER: US/08/076,726 E: 14-JUN-1993 TION: 435 TION: 435	CORRESPONDENCE ADDRESS: ADDRESSE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, N.W. CITY: Washington STATE: District of Columbia COUNTRY: United States of America ZIP: 20005-3934 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PatentIn Release #1.0, Version #1.25	1 2.08-076-726-16 STANDARI XXXXX equence 16, Application equence 16, Application atent No. 5464758 GENERAL INFORMATION: APPLICANT: BUJACT, M APPLICANT: B

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Query Match
Best Local S
Matches 42
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                                                                                                                                                                                                                                Patent No. 5650298
GENERAL INFORMATION:
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                                                                                                                     TITLE OF INVENTION: Tight Control of Gene Expression TITLE OF INVENTION: Cells by Tetracycline-responsive NUMBER OF SEQUENCES: 10
                                                                                                                                                                    APPLICANT: Salfeld, Joch
APPLICANT: Voss, Jeffrey
                                                                                                                                                                                                  APPLICANT:
                                                                                                       CORRESPONDENCE ADDRESS:
                              STATE: M
                                                                                                                                                                                                                                                                                                                                                                                   gtgtatgacctgctgctggagatgctgaatgcccac 1587
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                                                                                          ADDRESSEE:
                   02109-1875
                                                              Boston
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Application US/08260452
                                               Massachusetts
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                                                                            60 State Street
                                   USA
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Salfeld, Jochen
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Pred. No. 2.47e-138;
0; Mismatches 209;
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TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4963 base pairs
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TOPOLOGY: circ
MOLECULE TYPE: D
ORIGINAL SOURCE:
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Local Similarity 66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Giulio A. DeConti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC com
OPERATING SYSTEM: PC
SOFTWARE: ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCCACCTTCTAGAATGTGCCTGGCGTAGAGATCCTGATGATTGGTCTCGTCTGGCGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                              ACCCTGCAGCAGCAGCAGCGGCGGGCGGGCCCAGCTCCTCCTCATCCTCTCCCCACATCAGG
                                                                                                                                                                                                                                                                   CGCATGATGAATCTGCAGGGAGGAGGAGTTTGTGTTGCCTCAAATCTATTATTTTGCTTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-013CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
    catgcgagtaacaagggcatggaacatctgctcaacatgaagtgcaaaaatgtggtccca
                                   CACATGAGTAACAAAGGCATGGAGCATCTGTACAGCATGAAGTGCAAGAACGTGGTGCCC
                                                                                                                         tcacttg--ctgaacgccgtgaccgatgctttggtttgggtgattgccaagagcggcatc
                                                                                                                                                       TCTGGAGTGTACACATTTCTGTCCAGCACCCTGAAGTCTCTGGAAGAAGAAGGACCATATC
                                                                                                                                                                                                                                                  cgagagttaaaactccaacacaaagaatatctctgtgtcaaggccatgatcctgctcaat
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                                                                                                                                                                                                                                                                                                                                                                                                                                    gtgcggctcttggagagctgttggatggaggtgttaatgatggggctgatgtggcgctca
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                                                               tcctcccagcagcaatccatgcgcctggctaacctcctgatgctcctgtcccacgtcagg
                                                                                                                                                                                     tccagtatgtaccctctggtcacagcgacccaggatgctgac-agcagccggaagctggc
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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31,503
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Pred. No. 2.47e-138;
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Sequence 1, Applic
Patent No. 5550024
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                                                                                                                                                                                            TELEPAX: 515-288-1330
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3460 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Relea
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/I
FILING DATE: 26-SEP-199
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,71
          NAME/KEY: misc_feat
LOCATION: 1197..119
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: exon
                                                                                   HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE: NISC_feature
NAME/KEY: misc_feature
LOCATION: 303..304
OTHER INFORMATION: /note
OTHER INFORMATION: undet
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/961,819
FILING DATE: 19-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rothschild, Max F.
APPLICANT: Tuggle, Christopher K.
APPLICANT: Jacobson, Carol D.
                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: BF TELECOMMUNICATION INFORMATION:
                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Genetic Markers for Pig Litter Size NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                       STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Des Moines
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                                                                                                                                                                                           nucleic acid
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Application US/08312312A
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Plastow, Graham S.
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                                                                                                                                                              DNA (genomic)
                                                                                     /note= "Gap in DNA sequence
undetermined length"
                                undetermined
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                                                                                                                                                                                                                                                                                                                                us 07/687,708
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                                         /note= "Gap in DNA sequence
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2485 GCATTGTTGATAAAATCCGCAGGAAAAACTGCCCGGCGTGTCGCCTTAGAAAGTGCTGTC 2544
                                                                                                2365 TCTGTGGGGATGAAGCATCAGGCTGTCATTATGGTGTCCTCACCTGTGGGAGCTGTAAGG 2424
                                                                                                                                                                                        STRANDEDNESS: both
TOPOLOGY: both
SEQUENCE 6244 BP; 1483 A; 1749 C; 1610 G; 1402 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Applicat
Sequence 15, Applicat
Patent No. 5464758
GENERAL INFORMATION:
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CITY: Washington
STATE: District of Columbia
STATE: United States of America
COUNTRY: United States of America
ZID: 20005-3934
ZID: TOWNDABLE FORM:
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TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 4.2%;
Local Similarity 83.3%;
                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/O: FILING DATE: 14-JUN-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
                                          TCTTCTTTAAAAGGGCAATGGAAGGGCAGCATAACTATTTATGTGCTGGAAGAAATGACT 2484
                                                                                 tctgcagcgattacgcatcgggatatcactatggagtctggtcgtgtgaaggatgtaagg 604
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                           ccttttttaaaagaagcattcaaggacataatgattatatttgtccagctacaaatcagt 664
                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                 NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                          128;
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Similarity 66.3%;
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                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                    6244 base pairs
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1100 New York Avenue,
                                                                                                                                                                                                                                                                                                          (202)371-2600
(202)371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tight Control of Gene Expression in Eucaryotic Cells by Tetracycline-responsive Promoters
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ork Avenue, N.W.
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US/08076726
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Pred. No. 3.17e-29
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Pred. No. 2.34e-35
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                      2425 TCTTCTTTAAAAGGGCAATGGAAGGGCAGCATAACTATTTATGTGCTGGAAGAAATGACT 2484
                                                                   2365 TCTGTGGGGATGAAGCATCAGGCTGTCATTATGGTGTCCTCACCTGTGGGAGCTGTAAGG
                                                                                                                                    CLONE: pUHD BGR3
SEQUENCE 6244 BP; 1483 A; 1749 C; 1610 G; 1402 T; 0 OTHER
                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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APPLICATION NUMBER: 08/0
AFPORMATION INFORMATION:
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ADDRESSEE: Lahive & Cockfield
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: PUHD BG
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: ASCII text
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                                          tctgcagcgattacgcatcgggatatcactatggagtctggtcgtgtgaaggatgtaagg 604
                                                                                                                                                                      ORGANISM: Human cytomegalovirus STRAIN: Towne (hCMV)
                                                                                                                                                                                                                                                                                                                                      NAME: Giulio A. DeConti, Jr. REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
ccttttttaaaagaagcattcaaggacataatgattatatttgtccagctacaaatcagt
                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                           128;
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Similarity 66.3%;
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                                                                                                                                                                                                                     circular
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                                                           DNA (genomic)
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                                                                                                    Score 63; DB 1;
Pred. No. 3.17e-29
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                                                                                          Mismatches
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Best Local Similarity 1.4%;
Matches 5; Conservative
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                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                           TOPOLOGY: line
                                                                                                                                                                                                                                                                     FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
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TEX: 899149
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ctcccgcactcggggcgcgtggccgccacttctcttggccttgccggcacagtgcagctg 805
                                                            CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                      CLONE:
                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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Application
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8 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1800 Diagonal Road, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHEIFLINGER, F
                                                                                                                                                                                     7218 base pairs
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                                                                                           1.48;
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US/08232463
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205; M
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                                                                                           Score 62; DB 1; I
Pred. No. 1.82e-28;
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                                                                                   Mismatches 148;
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Sequence 14,
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INFORMATION FOR SEQ ID NO:
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                 Local Similarity
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APPLICANT:
                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 39,768
REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)83-4109
TELEFAX: (703)83-4109
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: EP 9.
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS AND SOFTWARE: Pathonia
                                                                                                                     STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                     linear
                                                                   1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
                                                                                                                                    single
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                  3.6%;
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   200;
                  Score 61; DB 1;
Pred. No. 1.04e-27
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Sequence 1, Application Sequence 1, Application Patent No. 5683885
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Query Match
Best Local Similarity
Matches 130; Conser
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Patent No. 5223606
APPLICANT: BLAUDIN DIERRE, DEJEAN, ANNE
TITLE OF INVENTION: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA NUMBER OF SEQUENCES: 11
                                                                       US-08-759-873-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3238
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                                                                                                                                                                                                                                  TAAGAACTGTGTTATTAATAAAAGTCACCAGGAATCGATGCCAATACTGTCGACTCCAGA
                                                                                                                                                                                                                                                                                                     ATGTAAGGGCTTTTTCCGCAGAAGTATTCAGAAGAATATGATTTACACTTGTCACCGAGA 679
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FILING DATE: 17-DEC-1987
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                                                                       STANDARD;
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                                                                       DNA; UNC;
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Pred. No. 3.26e-23;
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Best Local :
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                                                                                      Sequence 1, Application US/08629939
Sequence 1, Application US/08629939
Patent No. 5645995
                                                                                                                                                                                                                                                                                       2001
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                                                                                                                                                       US-08-629-939-1 STANDARD; DNA; UNC; 3014 BP
                                                                                                                                                                                                                                                                                                                                                                 545
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                                                                                                                                                                                                          725
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                                                               GENERAL INFORMATION:
APPLICANT: Kiebac
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TITLE OF INVENITATION.

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

STREET: 2100 Pennsylvania Avenue, N.W., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SULTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,873
FILING DATE: 12-APRIL-1996
CTACCTTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION IMPORMATION:
TELEPHONE: (202), 293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                         APPLICANT: Kieback, Dirk G.
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: RISK OF
NUMBER OF SEQUENCES: 14
                CORRESPONDENCE ADDRESS:
                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                    AGGCTGGCATGGT 2073
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Similarity 63.7%;
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  SUGHRUE, MION,
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METHODS FOR DIAGNOSING AN INCREASED RISK
OF BREAST OR OVARIAN CANCER
14
                         METHODS FOR DIAGNOSING AN INCREASED RISK OF BREAST OR OVARIAN CANCER 14
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Pred. No. 9.86e-22;
0; Mismatches 70; Indels
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    MACPEAK & SEAS
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Best Local
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           Query Match
Best Local Similarity
Matches
                                                                                                                  Patent No. 5260432.

Patent No. 5260432

Patent No. 5260432

Patent No. 5260432

Patent No. 5260432

TAKAKU, FUMIMARO; ISHIKAWA, TAKASHI; IMAWARI, MICHIO; EYANS, RONALD M.; UMESONO, KAZUHIKO

TITLE OF INVENTION: HUMAN GAMMA RETINOIC ACID RECEPTOR DNA NUMBER OF SEQUENCES: 4
                                                                    SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                        1881 TCTGTGGGGATGAAGCATCAGGCTGTCATTATGGTGTCCTTACCTGTGGGAGCTGTAAGG 1940
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                                             Sequence 1707
                                                                                                                                                                                           01-JAN-1900
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/629,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                             aagtgggaatggt 737
                                                                                                                                                                                                                                                                                                            gtacaatcgataaaaaccggcgcaagagctgccaggcctgccgacttcggaagtgttacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                              FILING DATE: 22-JUN-1989
                                                                                                                                                                                                                                                                                                                                    GCATCGTTGATAAAATCCGCAGAAAAAACTGCCCAGCATGTCGCCTTAGAAAAGTGCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                             LENGTH: 1576 nce 1707 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 3.1%;
Similarity 63.7%;
123; Conservative
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 Conservative
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                                             346 A; 478 C; 467 G;
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           3.0%;
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0; Mismatches
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           Score 51; DB 3; I
Pred. No. 2.91e-20;
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  Mismatches
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                                               285 T; 131 other;
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                       Length 1576;
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Matches 12
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Sequence 1, Application US/08087151
Patent No. 5468624
                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE 387 BP; 109 A; 92 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-087-151-1 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: E. Brad Thompson
APPLICANT: Lynne V. Nazareth
TITLE OF INVENTION: ANTI-TUMOR ACTIVITY OF A MODIFIED FRAGMENT
TITLE OF INVENTION: OF THE GLUCOCORTICOID RECEPTOR
NUMBER OF SEQUENCES: 3
                                                188 TCTGCCTGGTGTGCTCTGATGAAGCTTCAGGATGTCATTATGGAGTCTTAACTTGTGGAA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         652 CGAAGTGGGCATG
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                                                                                     Local Similarity les 126; Conser
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 512-320-7200
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: HOGGINS, Daniel S.
REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: UTSG:141/HOD
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
GCTGTAAAGTTTTCCTTCAAAAGAGCAGTGGAAGGACAGCACAATTACCTATGTGCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                     TELEPHONE: 512-474-7577
                                                                                                                                                                                                                                                                                                                                     FILING DATE: July 7, 1993
CLASSIFICATION: 1.2
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                                  tctgcgctgtctgcagcgattacgcatcgggatatcactatggagtctggtcgtgtgaag 595
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ZIP: 77210
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                                                                                     Conservative
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                                                                                                2.8%;
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                                                                                   Score 47; DB 1; I
Pred. No. 2.34e-17;
0; Mismatches 73
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                                                                                                                                                                                   MOLECULE TYPE: genomic SEQUENCE 387 BP; 109 A; 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-561-072-1 STANDARD; DNA; UNC; 387
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                                                                                                                                                                                                                                                   TELEX: NO. 5571791 Applicable INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
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                                                    248
                                                                                         188 TCTGCCTGGTGTGCTCTGATGAAGCTTCAGGATCTCATTATGGAGTCTTAACTTGTGGAA 247
308 GGAATGATTGCATCATCGCGATAAAATT-CGAAAAAACTGCCCAGCATGCCGCTATCGAA 366
                        596 gatgtaaggccttttttaaaaagaagcattcaaggacataatgattatatttgtccagcta 655
                                                                          536 tctgcgctgtctgcagcgattacgcatcgggatatcactatggagtctggtcgtgtgaag 595
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                                                                                                                                                                                                                                                                                                                                                     AFFLICATION NUMBER: 08/087,151
FILING DATE: July 7, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Hodgins, Daniel S.
REGISTRATION NUMBER: 31,026
REFERENCE TO TO TO THE TOTAL T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPEFFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,026
REFERENCE/COKET NUMBER: UT:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lynne V. Nazareth
TITLE OF INVENTION: ANTI-TUMOR ACTIVITY OF A MODIFIED FRAGMENT
TITLE OF INVENTION: OF THE GLUCOCORTICOID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                            GCTGTAAAGTTTTCTTCAAAAGAGCAGTGGAAGGACAGCACAATTACCTATGTGCTGGAA 307
                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 20
CLASSIFICATION:
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TELEFAX: 512-474-7577
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                                                                                                                                 126;
                                                                                                                                              2.8%;
Similarity 63.0%;
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Application
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Pred. No. 2.34e-17;
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                                                                                                                                 Mismatches
                                                                                                                                                                                    G; 98 T;
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                                                                                                                                                                                    0 OTHER.
                                                                                                                                 73;
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Sequence 3, Application PC/TUS9
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XXXXXX
                                                                                                                     SEQUENCE 2928 BP; 582 A; 1011 C; 789 G; 546 T; 0 OTHER
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           424
                                 538
                                           364 TGCTTTGTCTGTCAGGACAAGTCCTCAGGCTACCACTATGGGGTCAGCGCCCTGTGAGGGC 423
                                                                                                                                                                                                                                                    TELEFAX: (212) 644-0525
TELEX: (212) 422523 COO
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 675,08
FILING DATE: 22-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 673,83
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN PREGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: hRAR ALPHA
                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                NAME/KEY: CDS
LOCATION: 103..14
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
           TGCAAGGGCTTCTTCCGCCGCAGCATCCAGAAGAACATGGTGTACACGTGTCACCGGGAC 483
                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: sing
= = =
                              tgcgctgtctgcagcgattacgcatcgggatatcactatggagtctggtcgtgtgaagga 597
                                                                                                                                                                                                                                          LENGTH:
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Pred. No. 8.39e-14
0; Mismatches 7
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Search completed: Tue Job time: 79 secs.

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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5171671
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LENGTH: 2940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/
FILING DATE: 06-AUG-1990
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: RETINOIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGAACTGCATCATCAACAAGGTGACCCGGAACCGCTGCCAGTACTGCCGACTGCAGAAG 543
                                                            TGCTTTGAAGTGGGCATG 561
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tgttacgaagtgggaatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120;
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0; Mismatches 78;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Tue Nov 3 03:32:21 1998; MasPar time 2544.39 Seconds 1354.241 Million cell updates/sec

Tabular output not generated.

Title: >US-08-906-365-1 (1-1686) from US08906365.seq 1686

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 cagccattatacttgcccac......agaacccacagtctcagtga 1686 gtcggtaatatgaacgggtg......tcttgggtgtcagagtcact

Scoring table: TABLE default Gap 6

Nmatch STD: Dbase 0; Query 0

Searched: 552174 seqs, 1021863385 bases × N

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

Database:

emb155

1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om 7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro genbank107
12:gb_ba 13:gb_htg 14:gb_in 15:gb_om 16:gb_ov 17:gb_pat 18:gb_ph 19:gb_pl 20:gb_pr1 21:gb_pr2 22:gb_ro 23:gb_st 24:gb_sts 25:gb_sy 26:gb_un 27:gb_vi

Statistics: Mean 11.383; Variance 4.965; scale 2.293

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query	Length pa	D B	∄		
	00010	ייים רכוו	דיכווק כיי	. 6		pescription	Pred. No.
 4	1684	99.9	1740	21	AB006590	Homo sapiens mRNA for	0.00e+00
2	1683	99.8	2011	21	AF051427	sapiens estr	0.00e+00
ω	1496	88.7	2041	21	AF051428	sapiens	0.00e+00
4	1496	88.7	2745	21	AF060555	sapiens	0.00e+00
U	1495	88.7	3593	21	AB006589	sapiens	0.00e+00
σ	1452	86.1	1460	ဖ	A61586	Sequence 4 from Patent	0.00e+00
7	1450	86.0	1560	20	HSRNAERB	H.sapiens mRNA for est	0.00e+00
æ	1140	67.6	1650	22	RNAJ2602	Rattus norvegicus mRNA	0.00e+00
9	1136	67.4	2555	22	RNU57439	Rattus norvegicus estr	0.00e+00
10	1136	67.4	2568	9	A61583	Sequence 1 from Patent	0.00e+00
11	1036	61.4	1621	22	AF042058	Rattus norvegicus estr	0.00e+00
12	1021	60.6	2152	22	MMU81451	Mus musculus estrogen	0.00e+00
13	1010	59.9	1458	ဖ	A61588	Sequence 6 from Patent	0.00e+00
14	1010	59.9	1458	22	MMAJ220	Mus musculus mRNA for	0.00e+00
15	781	7	7	2	3 FO7 / FO0		000

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4	Sparus aurata estrogen	Rainbow trout estrogen	S.salar mRNA for oestr	H.sapiens mRNA for est	g	Homo sapiens estrogen	iens estro		Rat mRNA for estrogen	3	Taeniopygia guttata es	for c	Sequence 9 from patent	16	Sequence 1 from Patent	Human estrogen recepto	Sequence 1 from Patent	Chicken mRNA for estro	O.aries mRNA for estro		S.scrofa mRNA for estr	Oryzias sp. mRNA for e	Homo sapiens estrogen	C. jacchus mRNA for est	O	norvegicus	norvegicus	Rattus norvegicus mRNA		Rattus norvegicus mRNA
	170-11	.06e-12	.17e-12	.62e-12	.04e-13	.89e-13	.89e-13	2.54e-137	.54e-13	.54e-13	.21e-14	.59e-14	.59e-14	.59e-14	.59e-14	.59e-14	.59e-14	.73e-15	.73e-15	.57e-15	.57e-15	.17e-16	.57e-17	.76e-2	.93e-28					0.00e+00
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ALIGNMENTS

	CDS	source		TITLE JOURNAL	AUTHORS	MEDLINE	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	ACCESSION	DEFINITION	LOCUS	RESULT 1
/codon_start=1 /product="estrogen receptor beta" /broduct="estrogen receptor beta" /db_xref="pip:d1025978" /db_xref="pip:d1025978" /trans.lation="MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYYDSHHEYP /trans.lation="MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYYDSHHEYP AMTEYSPAYMNYSIPSNVTINLEGGPGROTTSPNVLWPTPGHLSPLVVHRQLSHLYAEP QKSPWCEARSLEHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYH YGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCG SRRERCGYKLVRRQRSADEQIHCAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAE	/organism="Homo sapiens" /db_xref="taxon:9606" 991691	11740	Ogawa, Saitama Medical School, Department of 2nd Blochemistry; 38 Morohongo, Moroyama, Iruma-gun, Saitama 350-04, Japan (E-mail:suogawa@saitama-med.ac.jp, Tel:81-492-76-1490, Fax:81-492-94-9751)	Direct Submission Submitted (13-AUG-1997) to the DDBJ/EMBL/GenBank databases. Sumito	2 (Σασες 1 CO 1/40) Ogawa, S.	98139878	Biochem. Biophys. Res. Commun. 243 (1), 122-126 (1998)	Ouchi,Y. and Muramatsu,M. The complete primary structure of human estrogen receptor beta (hER heta) and its because the complex of the compl	Ogawa, S., Inoue, S., Watanabe, T., Hiroi, H., Orimo, A., Hosoi, T.,	1 (sites)	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens		estrogen receptor beta.		mRNA for estrogen receptor beta, comp	AB006590 1740 bp mrNA PRI 27-FEB-1998	

BASE COUNT Query Match Best Local S Matches 168 661 601 606 541 546 481 486 421 426 361 366 301 306 241 246 181 186 121 126 841 721 726 666 781 786 61 66 μ. σ GGTCGGCAGACCACAAGCCCAAATGTGTTGTGGCCAACACCTGGGCACCTTTCTCCTTTA ATATACATACCTTCCTCCTATGTAGACAGCCACCATGAATATCCAGCCATGACATTCTAT CTTAATTCTCCTTCCTACAACTGCAGTCAATCCATCTTACCCCTGGAGCACGGCTCC TGCAAGGTGTTTTCTCAGCTGTTATCTCAAGACATGGATATAAAAAACTCACCATCTAGC AAGGCCTTTTTTAAAAGAAGCATTCAAGGACATAATGATTATATTTTGTCCAGCTACAAAT GGGAACCGTTGCGCCAGCCCTGTTACTGGTCCAGGTTCAAAGAGAGGGATGCTCACTTCTGC atatacataccttcctcctatgtagacagccaccatgaatatccagccatgacattctat cttaattctccttcctcctacaactgcagtcaatccatcttacccctggagcacggctcc tgcaaggtgttttctcagctgctatctcaagacatggatataaaaaactcaccatctagc CAGTGTACAATCGATAAAAACCGGCGCAAGAGCTGCCAGGCCTGCCGACTTCGGAAGTGT aaggccttttttaaaagaagcattcaaggacataatgattatatttgtccagctacaaat gctgtctgcagcgattacgcatcgggatatcactatggagtctggtcgtgtgaaggatgt GCTGTCTGCAGCGATTACGCATCGGGATATCACTATGGAGTCTGGTCGTGTGAAGGATGT gggaaccgttgcgccagccctgttactggtccaggttcaaagagggatgctcacttctgc AGCCCTGCTGATGAATTACAGCATTCCCAGCAATGTCACTAACTTGGAAGGTGGGCCCT ggccacgcgccccgagtgcgggagctgctgctggacgccctgagccccgagcagctagtg GGCCACGCGCCCCGAGTGCGGGAGCTGCTGCTGGACGCCCTGAGCCCCGAGCAGCTAGTG 99.9%; al Similarity 99.9%; 1685; Conservative 425 a PPHYLISRPSAPFTEASMAMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESC WMEVLAMSCIMMRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSRFSELKL OHKEYLCVKAMILLANSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKSGISSQQ QSMKLANLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAHVLRGCKSSIT GSECSPAEDSKSKEGSQNPQSQ"

3 463 c 459 g 393 t Score Pred. 0; M re 1684; DB 21; d. No. 0.00e+00; Mismatches 1; Length Indels 1740; 0 Gaps 425 245 120 125 60 65 545 485 420 360 365 300 305 180 185 600 605 480 665 540 840 845 780 785 720 725 660 0;

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CTCACCCTCCTGGAGGCTGAGCCGCCCCATGTGCTGATCAGCCGCCCCAGTGCGCCCTTC

965

KEYWORDS SOURCE ORGANISM

Homo

sapiens

Homo sapiens AF051427 g2970563

REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; primates; Catarrhini; Hominida 1 (bases 1 to 2011)
Moore, J.T., McKee, D.D., Moore, Slentz-Kesler, K., Horne, E.L.,

hordata; Vertebrata; Hominidae; Homo.

Mammalia; Eutheria;

.A., Su,J.-L., Lehmann,J.M. of.

and Estrogen

TITLE JOURNAL

Willson, T.M.

Cloning, Ligand Binding and Receptor beta isoforms Unpublished

Functional Activity Kliewer, S.A.,

Human

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98	2 AF051427 2011 bp mRNA pRI 19-MAR-19 N Homo sapiens estrogen receptor beta mRNA, complete cds. AF051427 Q2970563	SULT CUS CUS CESSION	RESU LOCU DEFI ACCE
	cagtga 1686	1681	Qy
	CAGTGA 1691	1686	ф
1680	tccgagtgcagcccggcagaggacagtaaaagcaaagagggctcccagaacccacagtct	1621	Qy
1685	TCCGAGTGCAGCCCGGCAGAAGAGGAAAAGCAAAAGAGGGCTCCCAGAACCCACAGTCT	1626	В
1620	ctgctgctggagatgctgaatgcccacgtgcttcgcgggtgcaagtcctccatcacgggg	1561	Qy
1625	CTGCTGCTGGAGATGCTGAATGCCCACGTGCTTCGCGGGTGCAAGTCCTCCATCACGGGG	1566	망
1560	aacaagggcatggaacatctgctcaacatgaagtgcaaaaatgtggtcccagtgtatgac	1501	Qy
1565	AACAAGGGCATGGAACATCTGCTCAACATGAAGTGCAAAAAATGTGGTCCCAGTGTATGAC	1506	В
1500	cagcaatccatgcgcctggctaacctcctgatgctcctgtcccacgtcaggcatgcgagt	1441	Qy
1505	CAGCAATCCATGCGCCTGGCTAACCTCCTGATGCTCCTGTCCCACGTCAGGCATGCGAGT	1446	Дb
1440	ctgaacgccgtgaccgatgctttggtttgggtgattgccaagagcggcatctcctcccag	1381	Qy
1445		1386	Db
1380	atgtaccetetggtcacagegacccaggatgctgacagcagcagcaggtggctcaettg	1321	Qy
1385	ATGTACCCTCTGGTCACAGCGACCCAAGCATGCTGACAGCAGCCGGAAGCTTGCTT	1326	Д
1320	ttaaaactccaacacaaagaatatctctgtgtcaaggccatgatcctgctcaattccagt	1261	Qy
1325	TAAAACTCCAACACAAAAAATATCTCTGTGTCAAGGCCATGATCCTGCTCAATTCCAGT	. 1266	DЪ
1260	gtagaaggaattctggaaatctttgacatgctcctggcaactacttcaaggtttcgagag	1201	Qy
1265	TAGAAGGAATTCTGGAAATCTTTGACATGCTCCTGGCAACTACTTCAAGGTTTCGAGAG	1206	Db
1200	cacccggcaagctcatctttgctccagatcttgttctggacagggatgaggggaaatgc	1141	Qy
1205		1146	Db
1140	ctcttggagagctgttggatggaggtgttaatgatggggctgatgtggcgctcaattgac	1081	Qγ
1145		1086	В
1080	atcagctgggccaagaagattcccggctttgtggagctcagcctgttcgaccaagtgcgg	1021	Qy
1085		1026	В
1020	accgaggcctccatgatgtccctgaccaagttggccgacaaggagttggtacacatg	961	Qy
1025		966	Db
960	ctcaccctcctggaggctgagccgcccatgtgctgatcagccgcccagtgcgcccttc	901	Qy

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Moore, J.T., McKee, D.D., Moore, Slentz-Kesler, K., Horne, E
Millson, T.M.
Direct Submission
Submitted (25-FEB-1998) M
Drive, RTP, NC 27709, USA
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//db_xref="plD:g2970564"
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//translation="mdlkNspsSLNspsSyNCSOSILpLEHGSIYIPSSYVDSHHEYP
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//translatichTpVNRETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYH
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//srrengradeglhunyicpAnnoxingsynchilese
//prvllsrpsApfteasmmMsLifklangchungsynchilese
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                  gccctgctgtgatgaattacagcattcccagcaatgtcactaacttggaaggtgggcctg
                                                                                 tatacatacetteeteetatgtagacageeaceatgaatateeageeatgacattetata
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Moore, J.T., McKee, D.D., M
Horne, E.L., Kliewer, S.A.,
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                                                                         GCCCTGCTGTGATTACAGCATTCCCAGCATGTCACTAACTTGGAAGGTGGGCCTG
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                                                                                                                   tatacataccttcctcctatgtagacagccaccatgaatatccagccatgacattctata
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1 (bases 1 to 27/45)

Moore, J.T., McKee, D.D., Slentz-Kesler, K., Moore, Su, J.L., Horne, E.L., Kliewer, S.A., Lehmann, J.M., Direct Submission

Submitted (20-APR-1998) Molecular Sciences, Glax
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//b_xref="publication="mdlknspsslnspssyncsosilplehgssyntshlyapp
//translation="mdlknspsslnspssyncsosilplehgssyntynthgushlyapp
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SRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAE
PPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKI PGFVELSLEPQUYLLLEAE
PPHVLISRPSAPFTEASMMSLTKLADKELVHMISWAKKI PGFVELSLEPQUYLLLEAE
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WMEVLAWGLWRASIDHPGKLIFAPDLVLDRDEGCVEGGILEIFDMLATTSRFREIKL
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SOURCE KEYWORDS ORGANISM

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receptor

Eukaryotae; Vertebrata; Homo sapiens

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Mosselman,S., Polman,J. and Ex beta: identification and estrogen receptor FEBS Lett. 392 (1), 49-53 (96354875)

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                                          GCTATGACATTCTACAGTCCTGCTGTGATGAACTACAGTGTTCCCGGCAGCAGCAGTAAC
                                                                                                                              aactcaccatctagccttaattctccttcctcctacaactgcagtcaatccatcttaccc
                                                                                                                                                                      AACTCACCGTCGAGCCTTAGTTCCCCTGCTTCCTATAACTGTAGCCAGTCCATCCTACCC
                                                                                                                                                                                                             tgtgcctcttcttgcaaggtgttttctcagctgctatc-tc--aagacatggatataaaa 105
                                                                                                                                                                                                                                  TGTACCTCTTCTCACAAGGAGTTTTCTCAGCTGCGACCCTCTGAAGACATGGAGATCAAA 69
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Submitted (17-APR-1997) Aldridge T.C., Molecular Endoc Group, ZENECA Central Toxicology Laboratory, Alderley Macclesfield, Cheshire SK10 4TJ, ENGLANG
3 (bases 1 to 1650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Direct Submission
Submitted (18-NOV-1997) Aldridge
Group, ZENECA Central Toxicology
Macclesfield, Cheshire SKIO 4TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue specific responses to estrogen: an exp differential activation of multiple estrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Vertebrata; Mammali
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 1650)
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Rattus norvegicus
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estrogen receptor
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larity 85.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Erbeta"
/note="The clone was isolated by RT-PCR from total RNA"
/note="The clone was isolated by RT-PCR from total RNA"
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/evidence=experimental
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AKRDAHFCAVCSDYASGYHYGVWPCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRK
SCQACRLRKCYEVGMYCGGSRERCGYRIVRRQSSSEGVHCLSAKRNGGHAPRVKE
LLLSTLSPEQLVLTLLEAEPBVLVSRFSMPTTESSMMSLTKLABKELVHMIGWAKK
IPGFVELSLLDQVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGI
LEIFDMELATTSRFRELKLQHKEYLCVKAMILLNSSMYELASANQEAESGRKLTHLLN
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LLLEMLNAHTLRGYKPSISGSECSSTEDSKNKESSQNLQSQ"
443 c 432 g 360 t
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/tissue_type="Prostate"
1. .1650
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ERbeta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
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                                                                                     TCAAGGTTCCGTGAGTTAAAACTCCAGCACAAGGAGTATCTCTGTGTGAAGGCCATGATC
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                                                             tcaaggtttcgagagttaaaactccaacacaaagaatatctctgtgtcaaggccatgatc
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                                                                                                                                                                                                                                                                                                           Submitted (03-MAY-1996) Eva L. NOVUM, Karolinska, Institute, Location/Qualifiers
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha;
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204 CCCATGAGTCTCTGAGAACATAATG-TC-CATCTGTACCTCTTCTCACAAGGAGTTTTCT 261 Local Similarity CAATCATCGCTCCTCTATGCAGAACCTCAAAAGAGTCCTTGGTGTGAAGCAAGATCACTA CAGCTGCGACCCTCTGAAGACATGGAGATCAAAAACTCACCGTCGAGCCTTAGTTC-CCT 320 GCCAGCCCTGTTACTAGTCCAAACGCAAAGAGGGATGCTCACTTCTGCCCCGTCTGCAGC ACAAGCCCAAATGTGCTATGGCCAACTTCTGGGCACCTGTCTCTCTTAGCGACCCATTGC GCTTCCTATAACTGTAGCCAGTCCATCCTACCCCTGGAGCACGGCCCCATCTACATCCCT 380 cccacgaatctttgagaacattataatgacctttgtgcctcttcttgcaaggtgttttct 75 GAAGCTGAACCAACCCAATGTGCTGGTGAGCCGTCCCAGCATGCCCTTCACCGAGGCCTCC CGGGTGAAGGAGCTACTGCTGAGCACCTTGAGTCCAGAGCAACTGGTGCTCACCCTCCTG AGTTCTAGCGAGCAGGTACACTGCCTGAGCAAAGCCAAGAGAAACGGTGGGCATGCACCC atggtgaagtgtggctcccggagagagagatgtgggtaccgccttgtgcggagacagaga ATGGTCAAGTGTGGATCCAGGAGAGAACGGTGTGGGTACCGTATAGTGCGGAGGCAGAGA gataaaaaccggcgcaagagctgccaggcctgccgacttcggaagtgttacgaagtggga GACAAGAACCGGCGTAAAAGCTGCCAGGCCTGCCGACTTCGCAAGTGTTATGAAGTAGGA aaaagaagcattcaaggacataatgattatatttgtccagctacaaatcagtgtacaatc AAAAGAAGCATTCAAGGACATAATGATTATATCTGTCCAGCCACGAATCAGTGTACCATA gattacgcatcgggatatcactatggagtctggtcgtgtgaaggatgtaaggccttttt GATTATGCATCTGGGTATCATTACGGCGTTTGGTCATGTGAAGGATGTAAGGCCTTTTTT gccagccctgttactggtccaggttcaaagagggatgctcacttctgcgctgtctgcagc GAGCACCCTTACCTGTAAACAGAGAGACACTGAAGAGGAAGCTTAGTGGGAGCAGTTGT cagttatcacatctgtatgcggaacctcaaaagagtccctggtgtgaagcaagatcgcta acaagcccaaatgtgttgtggccaacacctgggcacctttctcctttagtggtccatcgc atgaattacagcattcccagcaatgtcactaacttggaaggtgggcctggtcggcagacc ATGAACTACAGTGTTCCCGGCAGCACCAGTAACCTGGACGGTGGGCCTGTCCGACTGAGC tcctcctatgtagacagccaccatgaatatccagccatgacattctatagccctgctgtg TCCTCCTACGTAGACAACCGCCATGAGTATTCAGCTATGACATTCTACAGTCCTGCTG cagctgctatc-tc--aagacatggatataaaaaactcaccatctagccttaattctcct 132 ATGATGATGTCCCTCACTAAGCTGGCGGACAAGGAACTGGTGCACATGATTGGCTGGGCC gaggetgageegeecatgtgetgateageegeeceagtgegeeetteaeegaggeetee cgagtgcgggagctgctgctggacgccctgagccccgagcagctagtgctcaccctcctg agtgccgacgagcagctgcactgtgccggcaaggccaagagaagtggcggccacgcgccc Conservative 67.4%; Score 1136; DB 22; Pred. No. 0.00e+00; Mismatches Length 2555; Indels 6; Gaps 192 620 560 440 792 980 920 672 860 612 800 552 740 492 680 432 372 312 500 252 1220 1160 912 1100 852 1040 972 1032 5

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Eukaryota; Metazoa; Chord
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Patent number WO9709348-A/1,
KAROBIO AB (SE).
                                                                Sequence
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                                                              /organism="Rattus rattus"
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                             67.4%;
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ae; Murinae; Rattus.
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Petersen, D.N., Tkalcevic, G.T., Koza-Taylor,
                                                                                                                                                           Submitted (09-JAN-1998) Research, Eastern Point
                                                                                                                                                                                                           Identification of estrogen receptor estrogen receptor beta expressed in Endocrinology (1998) In press 2 (bases 1 to 1621)
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Location/Qualifiers
 /codon_start=1
/product="estrogen
                           /note="steroid hormone receptor"
                                     /gene="ERbeta"
                                                              /gene="ERbeta"
                                                                                         /db_xref="taxon:10116"
                                                                                                       /strain="Sprague-Dawley"
                                                                                                                  organism="Rattus norvegicus"
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GAGCAACTGGTGCTCACCCTCCTGGAAGCTGAACCACCCAATGTGCTGGTGAGCCGTCCC
                                       aagagaagtggcggccacgcgccccgagtgcgggagctgctgctggacgccctgagcccc
                                                              AAGAGAAACGGTGGGCATGCACCCCGGGTGAAGGAGCTACTGCTGAGCACCTTGAGTCCA
                                                                                                                               taccgccttgtgcggagacagagaagtgccgacgagcagctgcactgtgccggcaaggcc
                                                                                                                                                       TACCGTATAGTGCGGAGGCAGAGAAGTTCTAGCGAGCAGGTACACTGCCTGAGCAAAGCC
                                                                                                                                                                                                                     ccagctacaaatcagtgtacaatcgataaaaaccggcgcaagagctgccaggcctgccga
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/note="encodes U57439"
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LSLLDQVRLLESCMMEYLMVGLMWRSLDHPGKLIFA PODVULDEDEGKCVEGILEIFDM
LLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLASANQEAESSRKLTHLUNAVDEL
VWVIAKSGISSQQQSVRLANLLMLLSHVRHISNKGMEHLLSMKCKNVVPVYDLLLEML
NAHTLRGYKSSISGSECSSTEDSKNKESSQNLQSQ"
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/translation="mtfyspammysvpgstsnldggpvrQstspnvlwptsghlspl
AthcQssllyaeppkspwcearslehtlpvnretlkrklsgsscaspvtspnakrdah
fcavcsdyasgyhygwscegckaffkrsiqghndyiopatnqctidknrrkscQacr
lrkcyevgmvkcgsrrercgyrivrrqrssseqvhclskakrngghaprvkelllstl
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                                                                                                                                                                                                                                             Mus musculus
U81451
     murine estrogen 
Mol. Endocrinol.
                                                                    Tremblay, G.B.,
                                                                                                                          Eukaryotae;
Vertebrata;
                                                                                                                                                            Mus musculus
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                                                                                                                                                                                               chromosome 12.
                                                                                                                                                                                                               nuclear receptor;
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                                                                                                                                                                             mouse.
   estrogen receptor ndocrinol. 11 (3),
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Eutheria; Rodentia;
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estrogen
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   : beta
353-365
                                                                                                                                          eukaryotes;
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                                                    Copeland, N.G., Giguere, V.
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Sciurognathi; //

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(Estrb)
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                                    functional analysis
                                                                      Gilbert, D.
                                                                                                                                                                                                                                                                 mRNA,
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                                                                                                                        Murinae;
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TITLE
JOURNAL
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Best Local
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ACTTCGCAAGTGTTACGAAGTAGGAATGGTCAAGTGTGGATCCAGGAGAGAAAGGTGTGG
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                                                TCCAGCCACGAATCAGTGTACCATAGACAAGAACCGGCGTAAAAGCTGCCAGGCCTGCCG
                                                                                                                   CTGTGAAGGATGTAAGGCCTTTTTTAAAAGAAGCATTCAAGGACATAATGACTATATCTG
                                                                                                                                                                                      TGCTCACTTCTGCGCCGTCTGCAGTGATTATGCATCTGGGTATCATTACGGTGTCTGGTC
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Direct Submission
Submitted (09-DEC-1996) Molecular
Hospital, 687 Pine Avenue West, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="estrogen receptor beta"
//db_xref="plD:g1912468"
//db_xref="plD:g1912468"
//translation="mifyspavmnysvpsstgnleggpvrQtaspnvLwptsghLSpL
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FCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACR
LRKCYEVGMVKCGSRRERCGYRLVRRQRSASEO/HCLNKAKRTISGHTPRVKELLINSL
SPBQLVTLLLEAEPAVTLVSRSSMPFTEASMMYSLTKLADKELVHIGWAKKIFGFVE
LSLLDQVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFGM
LLATTARFRELKLQHKEYLCVKAMILLNSSMYPLATASQBAESSRKLTHLLNAVTDAL
VWVISKSGISSQQQSVRLANLLMLLSHVRHISNKGMEHLLSMKCKNVVPVXDLLLEML
NAHTLRGYKSSISGSECCSTEDSKSKESQNLQSQ"
49 a 526 c 570 g 507 t
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Eukaryotae; Metazoa;
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                                                   Submitted (15-JUL-1997)
Nutrition, Karolinska I
                                                                       Direct Submission
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estrogen receptor;
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//db_xref="piD:ei192418"
//db_xref="piD:ei2370297"
//db_xref="piD:g2370297"
//tans1ation="MAFYSPAVMNYSVPSSTGNLEGGPVRQTASPNVLWPTSGHLSPL
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FCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKNCQACR
LRKCYEVGMVKCGSRRERCGYRIVRRQRSASEQVHCLNKAKRTSGHTPRVKEILLNSL
SPEQLVTILLEAEPPNVLVSRPSMPFTEASMMMSLTKLADKELVHMIGWAKKIPGFVE
LSLLDQVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDM
LLATTARFREKLQHKEYLCVVAMILLNSSMYHLATASQEAESSRKLTHLNAVTDAL
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                                                                                                                                                                                                           AF074599
Homo sapiens
AF074599
                                      Brandenberger, A.W., Lebovic, D., Taylo
Direct Submission
Submitted (25-JUN-1998) Reproductive
University of California, San Francis
Francisco, CA 94143-0556, USA
                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammal primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1215)
Brandenberger, A. W., Lebovic, D., Taylor, R.N. and Homo sapiens estrogen receptor beta 5/6 splice v
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/organism="Homo sapiens"
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estrogen
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Db 781 G 781
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Search completed: Tue Nov 3 04:15:08 1998
Job time: 2567 secs.

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MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Tue Nov 3 04:51:42 1998; MasPar time 278.07 Seconds 824.913 Million cell updates/sec

Tabular output not generated.

Title: >US-08-906-365-1 (1-1686) from US08906365.seq

Description:
Perfect Score:
N.A. Sequence:
Comp: 1686

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Scoring table: TABLE Gap 6 default

Nmatch

STD:

Dbase 0; Query 0

Searched: 188442 seqs, 68026449 bases ×

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Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
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14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part20 31:part31 32:part32 33:part13
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 9.451; Variance 5.146; scale 1.837

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 12	3 5 5 7 7 10 10	Result No.
71 68	1434 1247 1247 1136 1010 197 197	Score 1667
4.2	85.1 74.0 74.0 67.4 59.9 11.7 11.7	Query Match 1 98.9 86.1
3460 2 2153	1434 1251 3 1257 3 2568 2 1458 2 4963 1 2092	
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WO9709348-A2.
13-MAR-1997;
09-SEP-1996;
08-SEP-1995;
15-MAR-1996;
11-APR-1996;
08-MAY-1996;
(KARO-) KARO
Enmark E, Gui
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Orghan receptor; oestrogen receptor beta; ER-
nuclear receptor; prostate cancer; benign pro
ovary cancer; cardiovascular Alecco-
powers continued to the continued to the
                                                                                                                                                                                                                           treating disease
Claim 6; Fig 13B; 45pp; English.

A cDNA clone (762843) codes for a novel human oestrogen recepto: related nuclear receptor (W13724), designated ER-beta. It was isolated from a human testis cDNA library using rat ER-beta cDN (see also T62842) as probe. The human ER-beta gene was mapped to chromosome 14 region 14q22-23. Rat, human and mouse ER-beta (W14723-25) can be used to isolate molecules for use in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
Key
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P-PSDB; W14724.
New isolated oestr
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Homo sapiens
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-1995; GB-018272.
(-1996; GB-005550.
(-1996; GB-007573.
-1996; GB-009576.
) KARO BIO AB.
E, Gustafsson J,
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enign prostatic
; osteoporosis;

    used to develop
osteoporosis or ca

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Query Match
Best Local Similarity
Matches 1455; Conse
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Sequence 1460 BP; 352 A: 370 C.
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larity 99.8%;
Conservative
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d. No. 0.00e+00;
Mismatches 3;
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                                           Query Match
Best Local Simil
Matches 1434;
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EP-798378-A2.
01-OCT-1997.
25-MAR-1997; 200903.
25-MAR-1996; EP-203284.
26-MAR-1996; EP-200820.
(ALKU ) AKZO NOBEL NV.
Dijkema R, Mosselman S;
WPI; 97-473188/44.
P-PSDB; W33212.
DNA encoding estrogen recidentify novel ligands of Claim 5; page 13-14; 45pg
                                                                                                                           DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues claim 5; Page 13-4; 45pp; English.

This sequence encodes a novel oestrogen binding protein. The cDNA sequence which encodes this protein can be alternatively spliced resulting in the detection of additional transcripts (see T88413) This receptor is able to bind and be activated by estradiol, esto estriol, can be used in a screening assay for the identification drugs e.g. novel ligands or hormonal analogues.

Sequence 1434 BP; 347 A; 373 C; 406 G; 308 T;
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estone; es
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estrogen receptor protein
en receptor protein; sterc
estriol; screening; ds.
                                           85.1%;
llarity 100.0%;
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                                         Score Pred.
                                         re 1434; DB 37;
1. No. 0.00e+00;
Mismatches 0;
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                                                                          DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues

PT identify novel ligands or hormonal analogues

PS Claim 5; Page 14-15; 45pp; Emglish.

CLaim 5; Page 14-15; 45pp; Emglish.

CC This partial sequence encodes a splice variant of a novel oestrogen binding protein, detected by screening a human testis cDNA library.

CC This protein contains an alternative exon 8 (exon 8B) of the novel coestrogen receptor represented in T88412. As a consequence of the control of this exon through an alternative splicing reaction, the reading frame encoding the novel receptor is immediately terminated, creating a truncation of the carboxy terminus of the novel receptor.

CC This novel receptor is able to bind and be activated by estradiol, estone and estriol, and can be used in a screening assay for the identification of new drugs e.g. novel ligands or hormonal analogues, however this contain an AF-2 region and therefore probably lacks the ability to modulate transcription of target genes in a ligand dependent
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196; EP-203284.

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IKZO NOBEL NV.

KZO NOBEL NV.
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25-MAR-1997; 200903.
22-NOV-1996; EP-2003284
26-MAR-1996; EP-200820
(ALKU ) AKZO NOBEL NV.
Dijkema R, Mosselman S
WPI; 97-473188/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues
Claim 5; Page 28-29; 45pp; English.
This sequence encodes splice variant of a novel cestrogen binding protein isolated from human thymus tissue. This protein contain an alternative exon 8 (exon 8C) of the novel cestrogen receptor represented in T88412.
This novel receptor is able to bind and be activated by estradiol, estone and estriol, can be used in a screening assay for the identification of new drugs e.g. novel ligands or hormonal analogues. This variant does not contain an AF-2 region and therefore probably lacks the ability to modulate transcription of target genes in a ligand dependent fashion.
Sequence 1257 BP; 297 A; 327 C; 355 G; 278 T;
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13-MAR-1997.
13-MAR-1996; E03933.
09-SEP-1995; GB-018272.
15-MAR-1996; GB-005550.
11-APR-1996; GB-007532.
08-MAY-1996; GB-009576.
08-MAY-1996; GB-009576.
(KARO-) KARO BIO AB.
Enmark E, Gustafsson J,
WPI; 97-19284217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         162842 standard; cDNA; 2568 BP.
T62842;
T62842;
08-JUN-1997 (first entry)
Rat oestrogen receptor beta (ER-beta) cDNA.
Orphan receptor; oestrogen receptor beta; ER-beta; nuclear receptor; prostate cancer; benign prostatic ovary cancer; cardiovascular disease; osteoporosis;
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CC A cDNA clone (T62842) codes for a novel rat oestrogen receptor-CC related nuclear receptor (W13723), designated ER-beta. A set of CC degenerate primers based on conserved sequences of the DNA-CC binding domain and ligand binding domain of nuclear receptors were CC used to amplify rat prostate cDNA. The PCR prod. was used to Screen a rat prostate cDNA library to obtain the ER-beta cDNA. CC This was then used to obtain human ER-beta cDNA (see also T62843) CC from a human testis cDNA library. Rat, human and mouse ER-beta CC (W14723-25) can be used to isolate molecules for use in the CC diseases, osteoporosis, prostate or ovarian cancer or benign CC prostatic hyperplasia and to test environmental chemicals for cestrogenic activity.

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A cDNA clone (T62844) codes for a novel mouse oestrogen receptor related nuclear receptor (W13725), designated ER-beta. Rat, hu and mouse ER-beta (W14723-25) can be used to isolate molecules use in the treatment of cardiovascular diseases, central nervousystem diseases, osteoporosis, prostate or ovarian cancer or be prostatic hyperplasia and to test environmental chemicals for oestrogenic activity.

Sequence 1458 BP; 365 A; 373 C; 403 G; 317 T;
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The minimal promoter PhCMV*-1 is based on the human CMV intermediate-early promoter (with enhancer region remover to a tetracycline operator, teto. The promoter is used express tTA transactivator in host cells. In clone pUHD (given in 076269), CDNA for rabbit progesterone receptor the control of PhCMV*-1.
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20-JUL-1993; JF-200333.
(MITU ) MITSUBISHI KASEI
WPI; 95-110650/15.
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Q85976;
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T42193 standard;
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encoded by the EAR-1r gene,
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Disclosure; Page 6; 8pp; Japanese
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oestrogen receptor; exon; polymorphism; allele; RFLP; litter riction fragment length polymorphism; Chinese; American; pCR; ification; polymerase chain reaction; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 7.5%;
Similarity 81.3%;
165; Conservative
                                                                                                                                                                                                                                                                                                            (first entry)
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/note= "undetermined length
between these nucleotides"
534..600
                                                                                                                                                Location/Qualifiers 303..304
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human; erb-A related ge
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gene, for
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Pred. No. 1.
0; Mismatc
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1.90e-71;
~as 38;
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gene; estrogen recept
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27-AUG-1996.
29-AUR-1991; 687708.
19-APR-1991; US-687708.
19-CTT-1992; US-961819.
26-SEP-1994; US-912312.
4 (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
A (IOMA) UNIV IOWA STATE RES FOUND INC.
A (IOMA) UNIV IOWA STATE RES FOUND INC.
                                                                                                              Query Match
Best Local
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ttcatcatgcccacttcgtagcacttgcgtagccggcaggc-tgacagctcttcctcctg
                                                                                       95;
                                                                                                              Similarity
                                                                                       Conservative
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/note= "binds
2011..2031
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2688..2693
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2636..2663
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2982..3002
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2922..2940
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2729..2755
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2146..2171
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                                                                                                              Score 71;
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6.97e-31
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Sequence 2153 BP; 445 A; 627 C; 624 G; 457 T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-1988;
23-0CT-1987; U02782.
4-0CT-1986; US-922585.
20-0CT-1987; US-108471.
(SALK) Salk Inst for Biol S
Evans RM, Weinberger CA, Ho
WPI; 88-133242/19.
                                                                                                                                                                                  PhCMV*1-controlled progesterone receptor tTA; transactivator; tetracycline-controllable transactivator; conditional inactivation; homologous recombination; gene expression; gene regulation; gene therapy; tetracycline-resistance; tetR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprising glucocorticoid, mineraloco and novel hormone receptors Claim 16; Fig V-2(B)-1 and -2; 243pp;
                                                                                                                                                                   gene regulation; gene therap
transgenic animal; PhCMV*-1;
                                                                                                                        Progesterone receptor;
                                                                                                                                                                                                                                                                                                                                                 Q76269 standard;
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N80922 standard; cDNA; 2153
N80922;
     (BADI )
                                                   14-JUN-1994;
                                                                            22-DEC-1994.
                                                                                                   WO9429442-A.
                                                                                                                                                                                                                                                                                              17-JUL-1995 (first entry)
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133; Conser
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Hollenberg
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Pred. No.
0; Misma
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                                                                                                                                                                        promoter;
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d. No. 8.56e-29;
Mismatches 65;
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Best Local S
Matches 12
                                                                                                                                                                       promoter linked to tet operon, and vectors and cells where gen expression is regulated by tetracycline Disclosure; Fig 9A-C; 37pp; English.

CDNA coding for the rabbit progesterone receptor was placed un control of the PhCMV*-1 promoter (see T0689), resulting in tetracycline-regulated expression vector pUHDpgr-3 contg. the sequence given in T06872. The construct was transfected into eukaryotic cells expressing the tTA transactivator (T06867) to allow tetracycline-regulated expression of the receptor.

Sequence 6244 BP; 1483 A; 1750 C; 1609 G; 1402 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5464758-A.
07-NOV-1995.
14-JUN-1993;
14-JUN-1993;
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T06872 standard; DNA; 6244 BP.
T06872;
2365 tctgtggggatgaagcatcaggctgtcattatggtgtcctcacctgtgggagctgtaagg 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PhCMV*-1 promoter and rabbit progesterone receptor.
Transactivator; tTA; tet operator; tet0; gene expression;
tetracycline-responsive promoter; PhCMV*-1; human cytomegalovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2545
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The minimal promoter PhCMV*-1 is based on the human CMV intermediate-early promoter (with enhancer region removed), fused to a tetracycline operator, teto. The promoter is used to express tTA transactivator in host cells. In clone pulb BGR3 (given in Q76269), CDNA for rabbit progesterone receptor is under the control of PhCMV*-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bujard H, Gossen M;
WPI; 95-392612/50.
Polynucleotide encoding trans:activator fusion protein contg. tet
repressor - used to control expression of gene regulated by minimal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BUJA/) BUJARD H.
(GOSS/) GOSSEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            725
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                                                                             y Match 3.7%;
Local Similarity 66.3%;
hes 128; Conservative
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US-076726.
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                                                                               No. 2.42e-25;
Mismatches 65;
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                                                                               Indels
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Qy 545 tctgcagcgattacgcatcgggatatcactattggagtctggtcgtggaaggatgtaagg 604

Db 2425 tcttctttaaaagggcaatggaagggcagcataactatttatgtgctggaagaaatgact 2484

Qy 605 ccttttttaaaagaagcattcaaggacataatgattatatttgtccagctacaaatcagt 664

Db 2485 gcattgttgataaaatccgcaggaaaaactgcccggcgtgtcgccttagaaagtgctgtc 2544

Qy 665 gtacaatcgataaaaaccggcgagcataatgattatatttgtccagcttagaaagtgctgc 2544

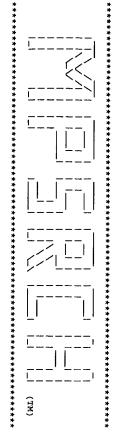
Qy 665 gtacaatcgataaaaaccggcgaggcactccggcgtgtcgccttagaaagtgttacg 724

Db 2545 aagctggcatggt 2557

Qy 725 aagtgggaatggt 737

Search completed: Tue Nov 3 04:56:31 1998

Job time: 289 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Nov 2 16:27:57 1998; MasPar time 27.56 Seconds 702.514 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score:

>US-08-906-365-2 (1-530) from US08906365.pep 3904 1 MDIKNSPSSLNSPSSYNCSQ......ECSPAEDSKSKEGSQNPQSQ 530

Scoring table: PAM 150 Gap 11

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 48.751; Variance 99.595; scale 0.489

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	, cs	4	ω	2		No.	Result
586	594	597	809	614	614	662	666	671	681	800	799	807	1473	1503	1516	1654	1663	1669	1683	1710	1735	3532	Score	
15.0	15.2	15.3	15.6	15.7		17.0	17.1	17.2		20.5		20.7	37.7	38.5	38.8	42.4		42.8		43.8	44.4	90.5	Match 1	Query
783	771	786	776	777	742	930	933	923	923	521	433	433	701	535	574	595	600	599	595	589	586	477	Length [
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A25691	A54273	A35466	S44047	QRHUGA	QRHUGB	A25923	QRHUP	153280	A39596	A29345	S58087	B29345	S64737	S58224	A37197	147140	QRRTE	QRMSE	QRHUE	QRCHE	QRXLE	S71400	ij	
	glucocorticoid recept	ro -		glucocorticoid recept	glucocorticoid recept	progesterone receptor	progesterone receptor	progesterone receptor	progesterone receptor	steroid hormone recep	estrogen receptor rel	steroid hormone recep	80K estrogen receptor		estrogen receptor - r	estradiol receptor -					estrogen receptor - A	estrogen receptor bet	Description	
	8.72e-88	2.25e-88	1.57e-90	1.04e-91	1.04e-91	3.61e-101	5.84e-102	5.99e-103	6.28e-105	1.24e-128	1.97e-128	4.93e-130	1.19e-265	7.90e-272	1.66e-274	5.58e-303	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	Pred. No.	

514	514	523	529	529	40 529 1	529	533	544	543	547	560	557	557	557	562	564	567	570	571	577	579	
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A47278	S26668	A29513	A41651	D41727	A34418	S26669	S37781	S60586	I51330	1HCQB	B34721	1HCP	1HCQE	1HCQA	A41401	A34721	A39248	B40494	A35895	QRRTG	S26595	
X rec	retinoic acid recepto	mineralocorticoid rec	retinoic acid recepto		on II	retinoic acid recepto	retinoid X receptor b	cep	androgen receptor - c		androgen receptor B -	humanCHICKEN ESTROGEN	humanCHICKEN ESTROGEN	Õ.	\sim				androgen receptor - m	glucocorticoid recept	estrogen receptor - b	
,	. 29e-		.10e-	.10€	.10∈	.10e-	. 86e-		7.84e-78	.31e-			1.48e-80	1.48e-80	1.57e-81	6.39e-82	1.66e-82	4.31e-83		1.85e-84	7.52e-85	

ALIGNMENTS

174 KRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQR 233	
121 KRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQR 180	
114 EHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFF 173	
61 EHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFF 120	
54 MNYSIPSNVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKSPWCEARSL 113	
1 MNYSIPSNVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKSPWCEARSL 60	
Query Match 90.5%; Score 3532; DB 2; Length 477; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Matc Best Local Matches
#length 477 #molecular-weight	SUMMARY
Cys) #status Cys) #status	96,99,113 132,138,1
<pre>#binding_site phosphate (Ser) (covalent) (by MAP kinase) #status predicted\</pre>	52
#region nuclear location signal\	167-182
#region zinc finger CCCC	132-156
355 #domain erbA transforming protein homology #label ERBA\	94-355 96-116
	FEATURE
steroid hormone receptor; transcription regulation; zinc finger	
DN	KEYWORDS
FICATION #superfamily estrogen receptor; erbA transforming protein homology	CLASSIFICATION
#cross-reference	##Cros
##TOLECULE_TYPE MKNA	##TPS1
. S7	#accession
FEBS LOTT: (1996) 592:49-53	#Journal
Mosselman, S.; Polman, J.; Dijkema, R.	#authors
U	REFERENCE
#IOTHEL_name Homo sapiens #Common_name man	DATE
	TITLE
S71400 #type complete	ENTRY
2	RESULT 1

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                                                                     Query Match
Best Local
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178-201
214-237
251-266
292-544
180,183,197,200
216,222,232,235
231
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                 70
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YSSASLSYAASSETEG-SSSLTGLHT-LNNVPPSSPVVELAKLPQLSPFIHHHGQQVFYYL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                         The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues.

In the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize discrete DNA sequences upstream of transcriptional start sites.

TION #superfamily estrogen receptor; erbA transforming protein
                                                   h 44.4%;
Similarity 50.8%;
247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Xenopus laevis estrogen receptor: sequence homology with human and avian receptors and identification of multiple estrogen receptor messenger ribonucleic acids.
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#formal_name Xenopus laevis #common_name African clawed
28-reb-1992 #sequence_revision 14-Jul-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                      DNA binding; nucleus; phosphoprotein;
steroid hormone receptor; transcrip
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Endocrinol. (
                                                                                                                                                                              #domain amino-terminal #label NH2\
#domain DNA binding #status predicted #label DNA\
#domain erbA transforming protein homology #label
#region zinc finger CCCC motif\
#region zinc finger CCCC motif\
#region nuclear location signal\
#omain steroid binding #status predicted #label S
#binding_site zinc (Cys) #status predicted\
#binding_site zinc (Cys) #status predicted\
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                                                       112;
                                                 Score 1735; DB 1; L
Pred. No. 0.00e+00;
112; Mismatches 107;
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#title
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#title :
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#cross-references MUID:88318621
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##status
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#accession S07192
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##residues
1-256,/E/,258-589 ##label KRU
##cross-references EMBL:X03805; NID:g63378; PID:g63380
##cross-references EMBL:X03805; NID:g63378; PID:g63380
NT The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues.

**YT In the absence of ligand, steroid hormone receptors are thought be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor appears to recognize discrete DNA sequences upstream of transcriptional start sites.
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                                                                                                                                                                                                                                                                  Krust, A.; Green, S.; Argos, P.
Bornert, J.M.; Chambon, P.
EMMO J. (1986) 5:891-897
The chicken oestrogen receptor
and the human oestrogen and g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maxwell, B.L.; McDonnell, D.P.; Conneel Greene, G.L.; O'Malley, B.W. Mol. Endocrinol. (1987) 1:25-35
Structural organization and regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        estrogen receptor - chicken
#formal_name Gallus gallus #common_name chicken
06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change
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                                                                                                                                                                                                                                                                                                                                              V.; Walter,
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REFERENCE
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Matches
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215,221,231,234
230,299
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177-450
177-200
177-235
213-235
250-265
                                                                   #journal
                  #cross-references
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#accession
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Local Similarity 51.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGIRKDRRGGRMMKQKRQREEQDSRNGEASSTELRAPTLWTSPLVVKHNKKNSPALSLTA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVGMMK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPQKSPWCEARSLEHTL-PVNRETLKRKVSGNRCASPVTGP-G--SKRDAHFCAVCSDYA
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                                                                                                                                                                                                                                                                                                                                   SGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAHVLRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ARFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEERDYIHRVLDKITDTLIHLMAK 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247;
                                                                                                                                                                                   QRHUE #type complete
estrogen receptor 1 - human
ER1; estrogen receptor alpha
#formal_name Homo sapiens #common_name man
28-May-1986 #sequence_revision 28-May-1986 #text_change
                                                     Shine, J.
Science (1986) 231:1150-1154
                                                                                                  Greene, G.L.; Gilna,
                                                                                                                      A94284
                                                                                                                                                       A94284; A93376; A43021; S27143;
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A94284
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                                               Sequence and expression of human
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finger
                complementary DNA
s MUID:86122927
                                                                                                                                     A03244; C41925; D41925
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#domain steroid binding #status predicted\
#binding_site zinc (Cys) #status predicted\
#binding_site zinc (Cys) #status predicted\
#binding_site phosphate (Ser) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #domain amino-terminal #label NH2\
#domain DNA binding #status predicted #label DNA\
#domain erbA transforming protein homology #label ERBA\
#region zinc finger CCCC motif\
#region zinc finger CCCC motif\
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d hormone receptor; transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #molecular-weight 66773 #checksum 793
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Pred. No. 0.00e+00;
112; Mismatches 99
                                                                                                  P.; Waterfield,
                                                                                                                                                       S34000; A41925; B41925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99;
                                               estrogen receptor
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                                                                                                  COMMENT
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                                               COMMENT
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DATE

ENTRY

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#title Human oestrogen receptor cDNA:
homology to v-erb-A.
#cross-references MUID:86146892
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##note sequence extracted from NCBI backbone (NCBIN:106597)

WIT The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues.

WIT In the absence of ligand, steroid hormone receptors are thought be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor compappears to recognize discrete DNA sequences upstream of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 216-254,367-399,'G',401-434 ##label PFE ##cross-references EMBL:X73067; NID:g579865; PID:g939886 ##note the authors translated the codon GGG for Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type mRNA
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##cross-references GB:M12674;
                                                                                                                                                                                                                                         ##molecule_type mRNA
##cross-references GB:M69296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-214,'ELPTLC' ##label DOT
##cross-references GB:M69297; NID:g182218; PID:g182219
##experimental_source clone 4; breast cancer
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                                                                                                                                                                                                                 ##experimental_source clone 24; breast cancer
                                                                                                                                                                                                                                                                                               ##status
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##cross-references GB:X03635; NID:g31233;
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Characterization of estrogen receptor variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfeffer, U.: Fecarotta, E.: Castagnetta, L.; Vidali, G. Cancer Res. (1993) 53:741-743
Estrogen receptor variant messenger RNA lacking exon 4
estrogen-responsive human breast cancer cell lines.
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Genomic organization of the human oestrogen receptor A43021
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Sequence analysis of the 5' flanking
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                                                                                                                                                                                                                                                                                                                       B41925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human breast cancers.
                                                                                                                                                                                                                                                                                                                                          the complete sequence of neither the nucleotide nor protein is shown in this paper sequence extracted from NCBI backbone (NCBIN:106580)
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'P',462-467;508-528 ##label PON
                                                                                                                                                                                                                                                                                            significant sequence differences
                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence has been revised after extraction
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NID:g182192; PID:g182193
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183-456
185-205
221-245
300-595
236,305
                                                                      #accession
                                                                                   #cross-references MUID:91042558
                                                                                                                           #journal
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##molecule_type mRNA
##residues 1-999 ##label WHI
##cross-references GB:M38651; NID:g193179; PID:g193180
##Cross-references and their receptors are invol
The steroid hormones and their receptors are invol
regulation of eukaryotic gene expression and aff
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QACRLRKCYEYGMMKGGIRKDRRGGRMLKHKRQRDDGEGRGEVGSAGDMRAANLWPSPLM
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                                                                                                                                                                                                                                                                                              YDLLLEMLNAHVLRGCKSSITGSECSPAEDSK-SKEGSQNPQS
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                                                                                                                                                                                                                                                                                                                                                                                                         MINWAKRVPGEVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPVKLLFAPNLLLDRNQGK 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V-RELL--LD-ALSPEQLVLTLLEAEPPHVLISR--PSAPFTEASMMSLTKLADKELVH
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Similarity 56.68;
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                                                                                                                                                                             #formal_name Mus musculus #common_name house mouse 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 05-Sep-1997
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receptor; transcription regulation;
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151/2; 215/1; 254/1; 366/1; 412/2; 457/1; 518/2
                                                                                                            Structural organization
                                                                                                                           White, R.; Lees, J.A.; Needham, M.; Ham, Mol. Endocrinol. (1987) 1:735-744
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187-460
187-210
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                                                                                                                                                                                                                                                                                                                 EHLLNMKCKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSQNPQS
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                                                                                                                                                                                                                                                                                                                                               EHLYNMKCKNVVPLYDLLLEMLDAHRLHAPASRMGVPPEEPSQTQLATTSSTSAHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGLLINLADRELVHMINWAKRVPGFGDLNLHDQVHLLECAWLEILMIGLVWRSMEHPGKL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKAKRSGG--HAPRV-RELLLD--ALS--PEQLVLTLLEAEPPHVLIS-RPSAPFTEASM
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Similarity 51.7%;
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n the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize discrete DNA sequences upstream of transcriptional start sites.
                                                     S07379;
S07379
Koike, S.; Sakai, M.; Muramatsu, M. Nucleic Acids Res. (1987) 15:2499-2513
                                                                                                   estrogen receptor - rat
#formal_name Rattus norvegicus
30-Sep-1991 #sequence_revision
05-Sep-1997
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Pred. No. 0.00e+00;
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                                                                                                                              #common_name Norway rat
14-Jul-1994 #text_change
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Best Local
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226,232,242,245
241,310
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188-461
188-211
224-246
261-276
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#cross-references MUID:87174780
#accession $07379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 SPSPLMLLHPPPHVSPFLHPHGHQVPYYLENEPSAY-AVRDTGPPAFYRSNSDNRRQNGR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##cross-references EMBL:X61098; NID:g56120; PID:g56121
The steroid hormones and their receptors are invo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                    LFAPNLLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTSPNVLWPTPGHLSP-LVVHRQLSHLYAEPQKSPWCEARSLEHTLPVNRETLKRKVSG-
                                                           MGLLTNLADRELVHMINWAKRVPGFGDLNLHDQVHLLECAWLEILMIGLVWRSMEHPGKL 407
                                                                                                                                                                                                                                                                                                ATNOCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADE-QLHCA-GK 244
                                                                                                                                                                                                                                                                                                                                                                            ATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDLEGRNEMGT
                                                                                                                                                                                                                                                                                                                                                                                                                                 NR-CASPVIGP----GSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERLSSSSEKGNMIMESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCP 227
EHLYNMKCKNVVPLYDLLLEMLDAHRLHAPASRMGVPPEEPSQSQLTTTSSTSAHS
                                  TATQDA-DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGM
                                                                                                                IFAPDLYLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLV
                                                                                                                                                                                            MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKL
                                                                                                                                                                                                                                                                           A--KRSGG--HAPRV-RELLLD--ALS--PEQLVLTLLEAEPPHVLIS-RPSAPFTEASM
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In the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize discrete DNA sequences upstream of transcriptional start sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                me steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maggi, A.M.A. submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA binding; nucleus; phosphoprotein; steroid binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.6%; Score 1663; DB 1; I larity 51.1%; Pred. No. 0.00e+00; Conservative 110; Mismatches 103;
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#domain erbA transforming protein homology #label
#region zinc finger CCCC motif\
#region zinc finger CCCC motif\
#region zinc finger CCCC motif\
#region nuclear location signal\
#domain steroid binding #status predicted #label S
#binding_site zinc (Cys) #status predicted\
#binding_site zinc (Cys) #status predicted\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Bokenkamp, D.; Jungblut, P.W.; Thole, H.H.
#journal Mol. Cell. Endocrinol. (1994) 104:163-172
#title The C-terminal of the porcine estradiol receptor contains no post-translational modification: determine of the primary structure.

#cross-references_MUID:95080454
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##residues
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                                                                                                                                                                                                                                                                                                 244 KA-KRSGG--HAPR-VRELLLDA--LS--PEQLVLTLLEAEPPHVLIS-RPSAPFTEASM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 SPSPLVLLHPPPQLSPFLHPHGQQVPYYLENEPSGY-AVREAGPPAFYRPNSDNRRQGGR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references EMBL:Z37167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                MGLLTNLADRELVHMINWAKRVPGFLDLSLHDQVHLLECAWLEILMIGLVWRSMEHPGKL 402
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EHLYNMKCKNVVPLYDLLLEMLDAHRLHA 551
                                     TATQDA-DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGM
                                                                                SSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHRRLAQLLLILSHFRHMSNKGM
                                                                                                                                                                                                                                                                                                                                       PGDMRSANLWPSPLLIKHTKKNSPVLSLTADQMISALLEAEPPIIYSEYDPTRPLSEASM 342
                                                                                                                                                                                                                                                                                                                                                                                 ATNOCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVR--RQRSADE-QLHCAG
                                                                                                                                                                                                                                                                                                                                                                                                                           ATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGEGRNEAVP
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Similarity 53.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thole, H.H.; Maschler, I.; Jungblut, P.W. Eur. J. Biochem. (1995) 231:510-516 Surface mapping of the ligand-filled C-terminal half of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain erbA transforming protein homology #label ERBA
#length 595 #molecular-weight 66361 #checksum 5521
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#formal_name Sus scrofa domestica #common_name domestic
21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
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estradiol receptor - pig
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297-307;310-313;320-323;329-332;337-340;417-420;466-473
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Pred. No. 5.58e-303;
97; Mismatches 90;
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REFERENCE A40070
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Best Local Similarity 56.3%;
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147-167
183-207
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#title Identification and estrogen induction of two
receptors (ER) messenger ribonucleic acids
trout liver: sequence homology with other E
#cross-references MUID:89127284
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##residues 150-574 ##label PA2
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##resid....
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                                                                       DCVEGMAEIFDMLLATVSRFGMLKLKPEEFVCLKAIILLNPGAFSFCSNSVESLHNSSAV 440
             ESMLDNITDALIHHISHSGASVQQQPRRQAQLLLLLSHIRHMSNKGMEHLYSIKCKNKVP 500
                                                                                                                                   HMIAWAKKVPGFQELSLHDQVQLLESSWLEVLMIGLIWRSIHCPGKLIFAQDLILDRSEG
AHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVP
                                                                                                                                                                                              SLNGGGGWRGPRITMPPEQVLFLLQGQTP-ALCSRQKVARPYTEVTMMTLLTSMADKELV 320
                                                                                                                   HMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEG
                                                                                                                                                                              RVREL--LLDA-LS-PEQLVLTLLEAEPPHVLISRPS-A-PFTEASMMMSLTKLADKELV
                                                                                                                                                                                                                                      RLRKCYEVGMYKCGSRRERCGYRLVRRQ-R---SA-D-EQLHCA-GKAKRS--GGH--AP 253
                                                                                                                                                                                                                                                       RLRKCYEVGMVKGGLRKDRGG-RVLRKDKRYCGPAGDREKPTVTWSTGQRPQDGGRNSSS 261
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                                                         KCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA-DSSRKL
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#region zinc finger
#length 574 #molecular-weight 62871
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Full-length sequence and in vitro expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA binding; nucleus; steroid hormone receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #superfamily estrogen receptor;
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Valotaire, Y.
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A37197
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                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 1.66e-274;
78; Mismatches 75;
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#authors #journal

Pink, V.C

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S.Q.; Wolf, D.M.; Bilimoria,

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Nucleic Acids F A novel 80 kDa

Res. (:

estrogen receptor

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24:962-969

\$64737 #type complete 80K estrogen receptor - human #formal_name Homo sapiens #common_name man 28_Oct-1996_#sequence_revision 13-Mar-1997

#text_change

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##cross-references EMBL:X89959; NID:g929901;
#CICATION #superfamily estrogen receptor; estrog
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VYDLLLEMLNAHYLRGC-KSSITGSEC-SPAEDSKSKEGS 524
                                                                                 VPVYDLLLEMLNAHVLRGC-KSSITGSEC-SPAEDSKSKEGS
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                                                                                                                                                                                              KLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNV
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Wigham, T.
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$58224
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##note the nucleotide sequence was submitted to t
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CLASSIFICATION #superfamily unassigned erbA-related proteins;
transforming protein homology
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QVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSR
                             QMSLLQSAWMEILILGIVYRSLPYDDKLAYAEDYIMDEEHSRLV-GLLDLYRAILQLVRR 330
                                                                                                                                                                           MKCLKVGMLKEGVRLDRV--R-GGRQKY-KRRLDSENSPYLNLPISPPAKKPLTKIVS-N 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QMSLLQSAWMEILILGIVYRSLPYDDKLAYAEDYIMDEEHSRLV-GLLELYRAILQLVRR 330
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                                                                     QLVLTLLEAEPPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFD 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSR
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                                                                                                                                                                                                             HFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRL 206
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                                                                                                     -L-LGV-EQDKLYAM-PPNDIPEGDIKALTTLCELADRELVFLINWAKHIPGFPSLTLGD 271
                                                                                                                                        RKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPE 266
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nl Similarity 38.7%;
137; Conservati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsson, R.; Berkenstam, A. submitted to the EMBL Data Library, July 1995 Expression of a novel member of estrogen response element-binding nuclear receptors is restricted early stages of chorion formation during mouse
                                                                                                                                                                                                                                                                                                                                                                                                         steroid hormone receptor; zinc finger
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Pred. No. 1.97e-128;
85; Mismatches 110;
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REFERENCE A49074
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Best Local Similarity 39.9%;
Matches 141; Conservative
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##residues 166-169,'X',171-173 ##label
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                                                                                                                                                                                                                                                                                                           RLCLVCGDVASGYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKACQACRF
                                                                          RRLQALRLEREEYVLLKALALANSDSVHIEDEPRLWSSCEKLLH--EAL---LEYEAGRA
                                                                                                                                                                                      TKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLPFPG-P-FPAGPLAVAGGPRKTAAPV 291
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              GPGGGAERRAGRILLTLPLLRQTAGKVLAHFYGVKLEGKVPMHKLFLEMLEA
                                             SRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKS
                                                                                                        FDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATT
                                                                                                                                      SDQMSVLQSVWMEVLVLGVAQRSLPLQDELAFAEDLVLD-EEGARAAGLGELGAALLQLV
                                                                                                                                                                    EQLVLTLLEAEPPHVL-ISRPSAPFTEASMMSLTKLADKELVHMISWAKKIPGFVELSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             steroid hormone receptor ERR1 precursor - human estrogen related receptor #formal_name Homo sapiens #common_name man 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 12-Sep-197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *superfamily unassigned erbA-related transforming protein homology DNA binding; nucleus; steroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A49074
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Nature (1988) 331:91-94
Identification of a new
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                                                                                                                                                                                                                                                                                                                                                                                                                  zinc finger
#molecular-weight 55742
                                                                                                                                                                                                                                                                                                                                                                                                                                                 zinc
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Pred. No. 1.:
74; Mismatc
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L.24e-1;
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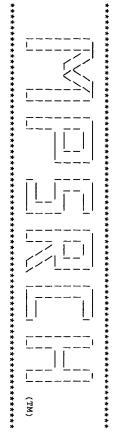
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FEATURE
555-819
557-577
593-617
                ACCESSIONS
REFERENCE
                                                                                        TITLE
ORGANISM
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REFERENCE
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #journal Schott, D.R.; Shyamala, G.; Schneider, #journal Biochemistry (1991) 30:7014-7020 #title Molecular cloning, sequence analyses, a complementary DNA encoding murine pro #cross-references MUID:91299759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
 #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mixing 1-923 ##label SCH ##restdues 1-923 ##label SCH ##cross-references GB:M68915; GB:J05333; NID:g200471; PID:g200472 ##cross-references GB:M68915; GB:J05333; NID:g200471; PID:g200472
                                                                                                                                                                                                                                     838
                                                                                                                                                                                                                                                                          372
                                                                                                                                                                                                                                                                                                              781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##status
                                                                                                                                                                                                 429 LLNAVTDALVWVIAKSGISSQQQSMRLANLL-MLLSHVRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.4%;
Local Similarity 30.8%;
les 123; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 PTPGHLSPLVVHRQLSHLYAEPQKSPWCEARSLEHTLP-VNRETLK-RKVSGNRCASPVT 138
                                                                                                                                            15
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                                                                                                                                                                                                                                                                                                                                              KKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDH-PGKLI-FAPDLVLDRDEGKCVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFDSLPQ-KICLICGDEASGCHYGVLTCGSCKVFFKRAMEGQHNYLCAGRNDCIVDKIRR 606
                                                                                                                                                                                                                                                                                           E-LSFYSLCLTMWQIPQEFVKLQVTHEEFLCMKVLLLLNT-I-PLEGLRSQSQFEEMRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                            FSPNQEIQLVP-PLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWS 723
                                                                                                                                                                                                                                   YIRELIKAIG-LRQKGVVPTSQRFYQLTKLLDSLHDLVKQ 876
                                                                                                                                                                                                                                                                         GILEIFDM-L-L-ATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAH
                                                                                                                                                                                                                                                                                                                                                                                KSLPGFRNLHIDDQITLIQYSWMSLMVFGLGWRSYKHVSGQMLYFAPDLILN-EQ-R-MK 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNCPACRIRKCCQAGMVI-GGRKFK-KFNKVRVMRTLDGVALPQSVGIPNESQALSQRIT 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRR 198
                                                                                                                                                                                                                                                                                                                                                                                                                     -ELLLDA-LSPEQLVLTLLEAEPPHVLISRPSA-PFTEASMMSLTKLADKELVHMISWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSCQACRIRKCYEVGMVKCGSRRERCGYRIVRRQRSADE-QI-HCAGKAKRSGGHAPRVR 256
                                           #type complete
progesterone receptor - rat
#formal_name Rattus norvegicus #
02-Aug-1996 #sequence_revision 0
25-Apr-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #region zinc finger\
#region zinc finger
#length 923 #molecular-weight 99073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A39596 #type complete
progesterone receptor B form - mouse
#formal_name Mus musculus #common_name house mouse
20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change
31_Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA binding; nucleus; steroid regulation; zinc finger
                I53280; B23733;
I53280
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Park-Sarge, O.K.; Mayo,
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#region zinc finger\
#region zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hormone receptor;
                                                                   #common_name Norway rat
02-Aug-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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FEATURE
555-819
557-577
593-617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #iournal Mol. Endocrinol. (1991) 5:967-978
#title Transient expression of progesterone receptor messenger RNA in ovarian granulosa cells after the preovulatory
#cross-references MUID:92049379
#accession B23733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 17.2%;
Best Local Similarity 32.6%;
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells.
#cross-references MUID:94130817
#accession I53280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #journal #title
                                                                                                                                                                                                                                                                                                                                                                            616
                                                                                                                                                                                                                                                                                                                                                                                                              847 G-LRQKGVVPSSQRFYQLTKLLDSLHDLVKQ 876
: |: ::| |: :|| | |::
                                                                                                                                                                                                                                                                                    674 VP-PLINLLMSIEPDVVYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNL 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA

##residues 555-589,'W',591-624;742-910 ##label PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **scatus preliminary; translated from GB/EMBL/DDBJ
*#molecule_type mRNA
##residence
                                                                                   380
                                                                                                                            789
                                                                                                                                                                  323
                                                                                                                                                                                                           733
                                                                                                                                                                                                                                             264 SPEQLVLTLLEAEPPHVLISRPSA-PFTEASMMMSLTKLADKELVHMISWAKKIPGFVEL 322
                                                                                                                                                                                                                                                                                                                             208 KCYEVGMVKCGSRRERCGYRLVRRQRSADE-QL-HCAGKAKRSGGHAPRVR-ELLLDA-L 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 1-923 ##label RES ##cross-references GB:L16922; NID:g463282; PID:g463283
                                                                                                                                                            VWVIAKSGISSQQQSMRLANLL-MLLSHVRH 467
                                                                               L-L-ATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDAL 437
                                                                                                        LTMWQIPQEFVKLQVTHEEFLCMKVLLLLNT-I-PLEGLRSQSQFEEMRSSYIRELIKAI 846
                                                                                                                                                                                                                                                                                                                                                                   KCCQAGMVL-GGRKFK-KFNKVRVMRALDGVALPQSVAFPNESQTLGQRITFSPNQEIQL 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #domain erbA transforming protein homology #label ERBA\
#region zinc finger\
#region zinc finger
#length 923 #molecular-weight 99407 #checksum 9843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA binding; nucleus; steroid hormone receptor; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endocrinology (1994) 134:709-718
Regulation of the progesterone receptor gene by gonadotropins and cyclic adenosine 3',5'-monophosphate in rat granulosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary; nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 671; DB 2; Length 923;
Pred. No. 5.99e-103;
94; Mismatches 108; Indels 21; Gaps
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Search completed: Mon Nov 2 16:30:48 1998 Job time: 171 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Nov 2 16:32:21 1998; MasPar time 40.39 Seconds 653.369 Million cell updates/sec

Tabular output not generated.

Title:

rfect Score:

>US-08-906-365-2 (1-530) from US08906365.pep 3904 1 MDIKNSPSSINSPSSYNCSQ......ECSPAEDSKSKEGSQNPQSQ 530

Scoring table: PAM 150 Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb16
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 49.103; Variance 84.403; scale 0.582

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

•		æ					
No.	Score	Query	Length	BB	Ħ	Description	Pred. No.
1	3564	91.3	549	11	035784	OESTROGEN RECEPTOR BET	T 0.00e+00
2	3532	90.5	477	4	~ 1	RECEPTOR E	
ω	3480	89.1	513	4	060685	ESTROGEN RECEPTOR BETA	A 0.00e+00
4	3476		495	4	809090	ESTROGEN RECEPTOR BET	A 0.00e+00
տ	3278	84.0	485	11	008537	RECEPTOR	⊅
თ	3274		485	11	Q62986	ESTROGEN RECEPTOR BETA	
7	3250	83.2	485	11	035635	ESTROGEN RECEPTOR, SUB	B 0.00e+00
8	3089		503	11	035785	OESTROGEN RECEPTOR BE'	T 0.00e+00
9	3076	78.8	503	11	070195	ESTROGEN RECEPTOR BETA	A 0.00e+00
10	2545		446	11	055015	ESTROGEN RECEPTOR BETA	A 0.00e+00
11	2347		464	11	055016	ESTROGEN RECEPTOR BET	A 0.00e+00
12	2240	57.4	573	13	013012	ESTROGEN RECEPTOR.	0.00e+00
13	1701		587	ű	Q91250	ESTROGEN RECEPTOR.	0.00e+00
14	1473	37.7	701	4	Q13511	80 KDA ESTROGEN RECEPT	T 0.00e+00
15	1227	31.4	307	13	091424	ESTROGEN RECEPTOR (FRA	A 1.08e-255
16	938	4	276	13	042174	ESTROGEN RECEPTOR (FRA	A 6.93e-186
17	816	20.9	481	4	Q14514	ESTROGEN RECEPTOR-RELA	1.
18	799	20.5	433	片	Q61539	ESTROGEN RECEPTOR RELA	_
19	765	19.6	159	σ	046402	ESTROGEN RECEPTOR ALPH	H 1.30e-144
20	760	19.5	420	11	008580	ESTROGEN RECEPTOR RELA	2

	45	44	43	42	41	40	39	38	37	<u>ა</u>	ω 5	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	
15	461	461	471	480	488	490	494	495	500	508	512	529	532	543	557	5.70	572	582	589	599	617	639	671	692	754	
	11.8	11.8	12.1	12.3	12.5	12.6	12.7	12.7	12.8	13.0	13.1	13.6	13.6			14.6	14.7	14.9	15.1	15.3	15.8	16.4	17.2	17.7	19.3	
	535 4	400 5	598 11				441 13			414 5								659 13		789 13	778 6		923 11		159 6	
	Q16311	061448	035865	P70052	Q91379	Q91840	Q90416	Q90415	Q64104	061449	073673	Q91425	019009	Q91445	Q14267	Q63049	Q13771	Q90946	008624	P70048	046567	042274	Q63449	Q95171	Q95131	
	TINUR= NGFI-B/NUR77 BE 7	RETINOID X RECEPTOR. 7	ORPHAN NUCLEAR HORMONE 4	ORPHAN NUCLEAR RECEPTO 3	NUCLEAR RECEPTOR TLX. 5	RETINOID X RECEPTOR BE 1	RETINOID X RECEPTOR AL 2	RETINOID X RECEPTOR. 1	MTLL=TAILLESS HOMOLOG. 9	RETINOID X RECEPTOR. 1	GLUCOCORTICOID RECEPTO 1	PROGESTERONE RECEPTOR 2	_	ANDROGEN RECEPTOR (FRA 1	ESTROGEN RECEPTOR-RELA 7	RAT ANDROGEN RECEPTOR. 7	ANDROGEN RECEPTOR. 2	PROGESTERONE RECEPTOR. 1	GLUCOCORTICOID RECEPTO 2	ANDROGEN RECEPTOR ALPH 1	GLUCOCORTICOID RECEPTO 8	PROGESTERONE RECEPTOR 6	PROGESTERONE RECEPTOR. 1		ESTROGEN RECEPTOR (FRA 5	
	7.57e-74	7.57e-74		3.63e-78	5.44e-80		2.32e-81	1.37e-81	9.85e-83	1.45e-84	1.76e-85	.18e-	4.45e-90	.30e-	7.59e-96	7.43e-99	2.55e-99			1.37e-105	8.74e-110	6.33e-115	1.99e-122	2.30e-127	5.26e-142	

ALIGNMENTS

Db	Qy E	2 X	# S	SQ	H	즣	XX	DR	DR	ᅜ	20	RĽ	RA	R A	RP	RN	뫈	RA	25	d X	8	88) G	DE	DT	Dī	멸	5 5	RESULT
80 STSNLDGGPVRQSTSPNVLWPTSGHLSPLATHCQSSLLYAEPQKSPWCEARSLEHTLPVN 139 : : : : :	1 MDIKNSPSSINSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTEYSPAVMNYSIPS 60	rvative 43; Mismatches 19; Indels 0; Gap	; Score 3564; DB 11; Length 549; ; Pred. No. 0.00e+00;	549 AA; 61325 MW; 7FB319E5 CRC32	CONFLICT 104 104 P -> S (IN REF. 2).	GER.	RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;	e_rec.	$\mathbf{-}$	EMBL; "AF042058; G2801691;	-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).	ENDOCRINOLOGY 0:0-0(1998).		PETERSEN D.N., TRALCEVIC G.T., KOZA-TAYLOR P.H., TURI T.G.,	SEQUENCE OF 65-549 FROM N.A.	[2]	SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.	ALDRIDGE T.C.;	STRAIN-WISTAR: TISSUE-PROSTATE:	CECUTENCE EBOX N >		EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	BATTIC NORVEGIOUS (BAT)	ECEPTOR BETA.		(TREMBLREL. 07,	01-JAN-1998 (TREMBLREI. 05, CREATED)	031/04 FREHELMART, FRI, 549 RA.	1 THE THINKS THE SAME SAME

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RESULT
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Best Loc
Matches
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MOSSELMAN S., POLMAN J., DIJKEMA R.;

FEBS LETT. 392:49-53(1996).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SI
EMBL; X99101; E255390; -

PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.

PFAM; PF00104; hormone_rec.

PFAM; PF00105; zf-c4.
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Q92731;
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EUKARYOTA; METAZOA; C
EUTHERIA; PRIMATES.
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01-FEB-1997 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                          LINC-FINGER
                                                                                                                                                                                                   RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
   181
                     174
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                             KRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQR
                                                         CKNVVPVYDLLLEMLNAHTLRGYKPSISGSECSSTEDSKNKESSQNLQSQ
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                  KRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQR
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Similarity 100.0%;
477; Conservative
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Pred. No. 0.00e+00;
0; Mismatches 0
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LAST ANNOTATION UPDATE)
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOORE J.T., MCKEE D.D., SLENTZ-KESLER K., MOORE L.B., SU J.L., HORRE E.L., KLIEWER S.A., LEHMANN J.M., WILI SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS:
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL, AF060555; G3091286; -.
EMBL, AF060555; G3091286; -.
EMBL, PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEINC-FINGER.
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATIC
ESTROGEN RECEPTOR BETA 3 ISOFORM.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUTHERIA; PRIMATES.
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Local Similarity 97.7%;
hes 470; Conservation
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                        VLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA
                                                                                                               LADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDL
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07, LAST SEQUENCE UPDATE)
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Pred.
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No. 0.00e+00
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PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

PROSITE; TRANSCRIPTION REGULATION; DNA-BINDING; NIRECEPTOR; NIRECEPTOR;
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O60608;
01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
ESTROGEN RECEPTOR BETAZ SPLICE VARIANT.
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EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
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OG2986;
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O1-NOV-1996 (TREMBLREL. C
O1-JUN-1998 (TREMBLREL. C
ESTROGEN RECEPTOR BETA.
RATTUS NORVEGICUS (RAT).
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EMBL; U81451; G1912468; -.
MGD; MGI-109392; ESTRB;
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
PFAM; PF00104; hormone_rec.
PFAM; PF00105; zf-C4.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
ZINC-FINGER.
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ESTRB.
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EUKARYOTA; METAZOA;
EUTHERIA; RODENTIA.
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01-JUL-1997 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
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NATURE 11:353-365(1997).
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TREMBLAY G.B.,
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Similarity 88.9%;
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Pred. No. 0.00e+00;
34; Mismatches 20
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EUTHERIA; I
[1]
                                                         ESTROGEN RECEPTOR, SU
MUS MUSCULUS (MOUSE)
EUKARYOTA; METAZOA; C
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PFAM; PF00105; zf-C4.
RECEPTOR; TRANSCRIPTION REGULATION;
ZINC-FINGER.
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-!- SUBCELLULAR LOCATION: NUCLEAR (IEMBL; U57439; G1373281; -.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
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KUIPER G.G.J.M., ENMARK
GUSTAFSSON J.A.;
PROC. NATL. ACAD. SCI. U
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SEQUENCE FROM N.A.

PETTERSSON K., GRANDIEN K., KUIPER G.G., GUSTAFSSON J

PETTERSSON (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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NUCLEAR (BY SIMILARITY).
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BETA.
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Pred. No. 0.00e+00;
35; Mismatches 20;
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EUKARYOTA;
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PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
PFAM; PF00104; hormone_rec.
PFAM; PF00105; zf-C4.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
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02-STROGEN RECEPTOR BETA2)
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ZINC-FINGER.
ENDOCRINOLOGY 0:0-0(1998)
-!- SUBCELLULAR LOCATION:
EMBL; AJ002603; E1184907;
                        PETERSEN D.N.,
BROWN T.A.;
                                                                           STRAIN-WISTAR;
ALDRIDGE T.C.;
                                         STRAIN=SPRAGUE-DAWLEY;
                                                 SEQUENCE FROM
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Pred. No. 0.
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01-AUG-1998 (TREMBLREL. 07, L
01-AUG-1998 (TREMBLREL. 07, L
ESTROGEN RECEPTOR BETA 2.
RATTUS NORVEGICUS (RAT).
EUKARYOTA: METAZOA; CHORDATA;
                   RECEPTOR; TR
ZINC-FINGER.
SEQUENCE 5
                                                                                                                                                                                                         070195
                                    MARUYAMA K., ENDOH H., SASAKI-IWAOKA H., KANOU H., HASHIMOTO S., KATO S., KAWASHIMA H.; BIOCHEM. BIOPHYS. RES. COMMUN. 246:142-147(1998).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AB012721; D1026359; -.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; N
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PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
PFAM; PF00104; hormone_rec.
PFAM; PF00105; zf-C4.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
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                                                                                                                                                                                                                                                                                                                                                                              RSIDHPGKLIFAPDLVLDR---
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Similarity 85.9%;
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                                                                                                          TISSUE-OVARY;
                    8
                                                                                                                                               CHORDATA;
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 78
                    ME;
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Pred. No. 0.
34; Mismatc
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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 3076;
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DNA-BINDING;
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00e+00;
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                                                                                                                                                TETRAPODA;
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                                      NUCLEAR
Length
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                                                                                               SHIMAYA
                                                                                                                                                MAMMALIA;
 503;
                                      PROTEIN;
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Best Local S
Matches 39
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Matches
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ZINC-FINGER.
SEQUENCE 4
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055015;
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1: SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
EMBL; AF042060; G2801695; -.
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
ESTROGEN RECEPTOR BETA1
                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY;
PETERSEN D.N., TKALCEVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERBETA.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATTUS NORVEGICUS (RAT)
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YRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRP
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                                  MTFYSPAVMNYSIPSNVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKS 105
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393; Conser
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                                                                                                               65.2%;
llarity 81.0%;
Conservative
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. 06, LAST SEQUENCE UPD
. 06, LAST ANNOTATION U
1 DELTA3.
                                                                                                                                                                                                                                                                                                                                                    G.T.,
                                                                                                             Score 2545; DB Pred. No. 0.00e+34; Mismatches
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35; 1
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Mismatches 20;
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Best Local S
Matches 39
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055016;
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY EMBL; AF042061; G2801697; -...
PROSITE; P500031; NUCLEAR_RECEPTOR; 1.
RECEPTOR; TRANSCRIPTION REGULATION; DN ZINC-FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UF
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION
ESTROGEN RECEPTOR BETA2 DELTA3.
ERBETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PETERSEN D.N., TKALCEVIC G.T.,
      142
                                                                                         121
                                                                                                                                    106
                                               166
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Pred. No. 0.00e+00;
34; Mismatches 19;
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01-JUL-1997 (TREMBLREL. 07, LAST SEC
1 01-AUG-1998 (TREMBLREL. 07, LAST ANY
E ESTROGEN RECEPTOR.
SANGUILLA JAPONICA (JAPANESE EEL).
DE GUKARYOTA; METAZOA; CHORDATA; VERTI
COSTEICHTHYES; ACTINOPTERYGII; ANGU
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 31
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ZINC-FINGER.
573 /
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PFAM; PF00105; zf-C4.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
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013012
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MOL. CELL. ENDOCRINOL. 119:37-45(1996).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

EMBL; AB003356; D1020638; -.

PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
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TODO T.;
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TGSECSPAEDSKSKEGSQNPQSQ 530
INQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADE-QLH-CAG--
                          TNQCTIDKNRRKSCQACRLRKCYEVGMMKCGVRRERCTYRGARHRRMPHIRELAGTGGGA
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Similarity 58.9%;
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04, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
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Pred. No. 0.00e+00;
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Best Local
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901250; PRELIMINARY;
091250; O91250;
01-NOV-1996 (TREMBLREL. C
01-NOV-1996 (TREMBLREL. C
01-JUN-1998 (TREMBLREL. C
ESTROGEN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                 EMBL; L79911; G1449146; -
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
PFAM; PF00104; hormone_rec.
PFAM; PF00105; zf-C4.
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-HYPOTHALAMUS-PREOPTIC AREA;

JACOBS E.C., ARNOLD A.P., CAMPAGNONI A.T.;

J. STEROID BIOCHEM. MOL. BIOL. 59:0-0(0).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POEPHILA GUTTATA (ZEBRA FINCH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                      RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PASSERIFORMES
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                 'Match 43.6%; Score 1701; DB 13; Local Similarity 51.6%; Pred. No. 0.00e+00; les 247; Conservative 112; Mismatches 99;
                                                                                                                                                                                                                                                 YSSTTLSYAPTSESEG-SSSLAGFHS-LNSVPPSPVVFLQTAPHWSPFIHHHSQQVPYYL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKNVVPVYDLLLEMLNAHVLRGCKSSIT-GSECSP-AEDSKSKEGS
                                                                                                         GGIRKDRRGGRVMKQKRQREEQDSRNGEASSTELRAPTLWASPLVVKHNKKNSPALSLTA 304
                                                                                                                                                                                                    ENDQGSFGMREAAPPAFYRPNSDNRRHSIRERMSSANEKGSLSMESTKETRYCAVCNDYA 184
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                                              CGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRE--LLL----D--ALS--P
                                                                                                                                                    SGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVGMMK 244
                                                                                                                                                                                      EPQKSPWCEARSLEHTL-PVNRETLKRKVSGNRCASPVTGP-G--SKRDAHFCAVCSDYA
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE
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RESULT 14
ID Q13511;
AC Q13511;
AC Q13511;
DT Q1-NOV-1996 (TREMBLREL. 01, CFDT 01-NOV-1996 (TREMBLREL. 06, LFDT 01-JUN-1998 (TREMBLREL. 06, LFDT 01-JUN-1998)

CC EUKARYOTA; METAZOA; CHORDATA;
CC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST;
RX MEDLINE; 96174665.
RN NUCLEIC ACIDS RES. 24.962-969
CC -1-SUBCELLULAR LOCATION: NUCLEIC ACIDS RES. 24.962-969
CC -1-SUBCELLULAR LOCATION: NUCLEIC ACIDS RES. 24.962-969
CC EMBL; U47678; G1197855; -.
DR PROSITE; PS00031, NUCLEAR_REC.
DR PROSITE; PS00031, NUCLEAR_REC.
DR PRAM; PF00104; hormone_rec.
DR PFAM; PF00104; hormone_rec.
DR PFAM; PF00105; Zf-C4.
RW ZINC-FINGER.
SQ SEQUENCE 701 AA; 78430 MW;
RESULT
AC QS
DT 01
DT 01
DT 01
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Best Local S
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           Q91424;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUE
01-JUN-1998 (TREMBLREL. 06, LAST ANNOT
ESTROGEN RECEPTOR (FRAGMENT).
CNEMIDOPHORUS UNIPARENS.
EUKARYOTA; ANIMALIA; METAZOA; CHORDATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 96174665.

PINK J.J., WU S.Q., WOLF D.M., BILIMORIA M.M., JO NUCLEIC ACIDS RES. 24:962-969(1996).

-: SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY) EMBL; U47678; G1197855; -.

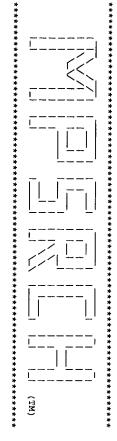
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

PFAM; PF00104; hormone_rec.

PFAM; PF00105; zf-C4.

RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
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701 AA;
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                                                                                                                                                                                                                                                                                                                                       MINWAKRVPGEVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPVKLLFAPNLLLDRNQGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARFRMMNLQGEEFVCLKSIILLNSGYYTFLSSTLKSLEEKDYIHRVLDKITDTLIHLMAK 484
:||| ::|| |::|:|:|:|| :::|
SRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAH-LLNAVTDALVMVIAK 443
                                                                                                                                                                                          HLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGM
                                                                                                                                                                                                                                                                                                                      {\tt MISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGK}
                                                                                                                                                                                                                                                                                                                                                                                                      IKRSKKNSLALSLTADQMVSALLDAEPP-ILYSEYDPTRPFSEASMMGLLTNLADRELVH
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                                                                                                                                                                                                                                                        CVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA-DSSRKLA
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l Similarity 56.9%;
197; Conservative
                                                                                                                              PRELIMINARY;
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Pred. No. 0.00e+00;
85; Mismatches 49
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LAST SEQUENCE UI
LAST ANNOTATION
     CHORDATA; VERTEBRATA; REPTILIA;
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                                                             SEQUENCE UP
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                                                                              UPDATE)
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                                                            UPDATE)
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Search completed: Mon Nov Job time: 232 secs.
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Best Local Similarity 56.7%;
Matches 174; Conservative
                                            467
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                              408
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                                                                                          HASNKGM 473
                      HMSNKGM 307
                             2 16:36:13 1998
                                                                                                          Score 1227; DB 13;
Pred. No. 1.08e-255;
68; Mismatches 53;
                                                                                                          Indels 12; Gaps
                                                                                                                  Length 307;
                                                                                                           10;
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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Nov 2 16:36:30 1998; MasPar time 7.02 Seconds 534.685 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-906-365-2 (1-530) from US08906365.pep 3904 1 MDIKNSPSSLNSPSSYNCSQ.....ECSPAEDSKSKEGSQNPQSQ 530

Scoring table: PAM 150 Gap 11

Searched: 77309 seqs, 7078906 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 33.550; Variance 151.595; scale 0.221

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score 1648 660 609 577	ry Len	1	DB 3	ID 5223606-5 5223606-6 5223606-7 US-07-716-	Description Patent No. 5223606. Patent No. 5223606. Patent No. 5223606. Sequence 5, Applicatio	Pred. 5.61 1.47 7.04
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7	514	. 2	467	1	US-08-336-	4.	icatio
8	514	.2	467	2	PCT-US91-0	4, Appl	icatio
9	513	<u></u> -	462	1	US-08-336-	Sequence 2, Applicatio	atio
10	513	<u>, , , , , , , , , , , , , , , , , , , </u>	462	N	PCT-US91-0	2	atio
11	486	. 4	463	_	US-08-336-	6,	atio
12	486	. 4	463	N	PCT-US91-0	σ	atio
13	441	.ω	454		5260432-2		•
14	439	.2	368		5223606-3	Patent No. 5223606.	•
15	439	11.2	448		5223606-2	No.	•
16	428		462		PCT-US92-0	,=	itio
17	428		797	N	PCT-US92-0	2	atio
18	420	œ	440	_	US-08-333-	φ,	icatio
19	420	œ	440	_	US-08-694-	8, Appl	atio
20	420	80	440	_	US-08-463-		atio
21	420		447	۲	US-08-373-		atio
22	413	o	462	ω	5171671-2		•
23	378	. 7	472	سر	US-08-496-	Sequence 2, Applicatio	atio

365 9.3 348 1 US-07-843- Sequence 10, Applicati 7.68e-22 365 9.3 348 1 US-08-459- Sequence 10, Applicati 7.68e-22 365 9.3 348 1 US-08-459- Sequence 10, Applicati 7.68e-22 365 9.2 414 1 US-08-255- Sequence 9, Applicatio 3.20e-21 361 9.2 469 2 PCT-US95-1 Sequence 2, Applicatio 1.74e-21 357 9.1 89 1 US-08-687- Sequence 3, Applicatio 3.92e-21 357 9.1 89 1 US-08-851- Sequence 3, Applicatio 3.92e-21 357 9.1 89 1 US-08-51- Sequence 1, Applicatio 3.92e-21 359 9.0 484 2 PCT-US95-1 Sequence 1, Applicatio 8.85e-21 349 8.9 66 3 5217867-1 Patent No. 5217867. 2.00e-20 329 8.4 451 2 PCT-US95-1 Sequence 2, Applicatio 1.15e-18 315 8.1 70 1 US-07-737- Sequence 3, Applicatio 1.09e-17 307 7.9 446 1 US-08-342- Sequence 3, Applicatio 9.64e-17 310 7.9 461 1 US-08-330- Sequence 2, Applicatio 5.28e-17 310 7.9 461 1 US-08-330- Sequence 2, Applicatio 5.28e-17 310 7.9 461 1 US-08-330- Sequence 2, Applicatio 5.28e-17 310 7.9 461 1 US-08-331- Sequence 2, Applicatio 5.28e-17 309 7.9 548 1 US-08-694- Sequence 2, Applicatio 6.45e-17 309 7.9 548 1 US-08-634- Sequence 2, Applicatio 6.45e-17 309 7.9 548 1 US-08-634- Sequence 2, Applicatio 6.45e-17 304 7.8 558 1 US-08-635- Sequence 12, Applicati 1.76e-16 304 7.8 558 1 US-08-333- Sequence 12, Applicati 1.76e-16	45	44	4 3	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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റ്റ	APPLICANT: BLAUDIN DE THE, HUGHES; MARCHIO, AGNES; TIOLLAIS,
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ဂ	TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED
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င္ပ	CURRENT APPLICATION DATA:
38	APPLICATION NUMBER: US/07/134,130
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SQ	SEQUENCE 444 AA; 50020 MW; 1110634 CN;
Query Best Matc)	Query Match 42.2%; Score 1648; DB 3; Length 410; Best Local Similarity 56.9%; Pred. No. 5.61e-141; Matches 224; Conservative 92; Mismatches 64; Indels 14; Gaps 11;
Db	1 CAVCHDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRK 60
Qy	149 CAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRK 208
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Qy	209 CYEVGMVKCGSRRERCGYRLVRRORSADE-QLHCAGKA-KRSGGHAP-RV-RELL- 259
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Qy	260 -LD-ALSPEQLVLTLLEAEPPHYLISRPSAPFTEASMMSLTKLADKELVHMISWAKKIP 317
Db	181 GFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPVKLLFAPNLLLDRNQGKCVEGMVEIF 240
Qy	318 GFYELSLFDQVRLLESCWMEVLMWGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIF 377
Db	241 DMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDT 300
Qy	378 DMLLATTSRFREIKLQHKEYLCVKAMILLNSSMYPLVTATQDA-DSSRKLAHLLNAVTDA 436

Gaps

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                              Patent No. 522:
APPLICANT:
              PIERRE; DEJEAN,
                                                                                          Patent No.
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CURRENT APPLICATION DATA:
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CE 393 AA; 44638 MW; 907537 CN;
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CURRENT APPLICATION DATA:
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APPLICANT: Simons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CLVCSDEASGCHYGVLTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRYRK
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                          SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
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                                                                      CLASSIFICATION:
                                                                                          APPLICATION NUMBER: FILING DATE: 19910
                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 20036-5601
                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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              REGISTRATION NUMBER:
                                  NAME:
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                                Scott,
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Eleventh floor,
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Garabedian, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto,
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                                                                                    UMBER: US/07/716,827C
19910619
                                  Watson
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7: 26,581
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ti, P. K.
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Pred. No. 7.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)8613000
TELEFAX: (202)82-8944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   XXXXX
                                                                                                                                                                                                                                                                           Sequence 2,
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                                                                                                                                                                                                                                                      Sequence 2, Application
                                                                                                                                                                                                                                               Patent No.
                                                                 ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vecurrent Application Data:
                                                                                                                                                                                                                                   GENERAL INFORMATION:
        ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A
REGISTRATION NUMBER: 31,677
                                                                                                                                                                                                       TITLE OF INVENTION: A NEW MEMBER OF THE NUCLEAR HORMONE TITLE OF INVENTION: RECEPTOR SUPERFAMILY AND A CDNA CLO
                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                      SLPCMYDQCKHMLFVSSELQRLQVSYEEYLCMKTLLLLSS 692
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                                    APPLICATION NUMBER: US FILING DATE: 19920928 CLASSIFICATION: 435
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TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                               CITY: SAN FRANCISCO
STATE: CA
                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                          Application US/07952800
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llarity 32.98;
Conservative
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                                                                                                                                                                 TOWNSEND AND MARKET PLAZA,
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NUMBER:
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                                                         US/07/952,800
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15280-21-1
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Patent No. 1NFORMATION:
OZATO, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein FINCE 533 AA; 56921 MW;
                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                          COUNTRY: U:
ZIP: 94105
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                                                                                                                           STATE:
                                                                                                                                                        STREET:
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                                                                                                                                                                     ADDRESSEE:
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Similarity 34.1%;
                                                                                                                                                                                                                                                                                4, Application 
o. 5403925
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              Application US/07952800
                                                                                                                                        SAN FRANCISCO
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AMINO ACID
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                                                                                                                                                      E: TOWNSEND AND TOWNSEND
1 MARKET PLAZA, STEUART 1
                                                                                                         USA
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Pred. No. 6.07e-37;
85; Mismatches 132;
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                Version
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Query Match Best Local S Matches 12

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MOLECULE TYPE: SEQUENCE 446 AA;
                                                                                                                                                                                                                                                                                                                                                    US-08-336-408B-4
                                                                                                                                                                                                                                           Sequence 4, Application US/08336408B
                                                                                                                                                                                        Sequence 4, Application US/08336408E Patent No. 5723329
                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 IDTFLMEMLEAPHQL 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
                                                                                                                                                                        GENERAL INFORMATION:
                           CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN &
STREET: 444 SOUTH FLOWER STREET, SUITE 2000
                                                                          TITLE OF INVENTION: RETINOIS TITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 7
                                                                                                                APPLICANT: EVANS, RONALD M.
APPLICANT: MANGELSDORF, DAVID J.
TITLE OF INVENTION: RETINOID RECEPTOR COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                       VYDLLLEMLNA-HVL 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSA-GVGAIFDRVLTELVSKMRDMRMDKTELGCLRAIILFNPDAKGL-SNPGEVEI---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HISWAKKIPGEVELSLEDQVRLLESCWMEVLMMGLMWRSIDHPGKLIEAPDLVLDRDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APEEMPVDR-ILEAELAVEQKS-DQ-GVEGPGATGGGGSSP-NDP--VTNICQAADKQLF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKDCTVDKRQRNRCQYCRYQKCLATGM-K----RE--AVQ-EERQRGKDKDGDGDG-AGG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRGLHCPPPPGGPGAGK--RLCAICGDRSSGKHYGVYSCEGCKGFFKRTIRKDLTYSCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -R--EKVYASLE-TYCKQKYP-EQQG-RFAKLLLRLPALRSIGLKCLEHLFFFKLIGDTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KCVEGILEIFDMLLAT-TSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRPSAPFTEASMMMSLTKLADKELV 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 19920 CLASSIFICATION: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: AMINO ACID
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ilarity 34.1%;
Conservative
LOS ANGELES
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Pred. No. 1.40e-36;
84; Mismatches 133;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein SEQUENCE 467 AA; 51216 MW; 1083042 CN;
            Sequence 4, Application PC/TUS9100399
                                                                                 XXXXXX
                                                                                                                   PCT-US91-00399-4
                                                                                                                                                                                        446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 08-NOV-1994

PRIOR APPLICATION 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/933,453

PRIOR APPLICATION NUMBER: US 07/933,453

PRIOR APPLICATION NUMBER: WO PCT/US91/003:
APPLICATION NUMBER: WO PCT/US91/003:
APPLICATION NUMBER: US 07/478,071

PRIOR APPLICATION NUMBER: US 07/478,071

REGISTRATION NUMBER: 31,192

REGISTRATION NUMBER: P41 9851

TELEPHONE: 619-546-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     ISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNA
                                                                                                                                                                                                                     YP-EQPG-RFAKLLLRLPALRSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEA
                                                                                                                                                                                                                                                                                            KMRDMQMDKTELGCLRAIVLFNPDSKGLSNPA-EVEA---L-R--EKVYASLE-AYCKHK 412
                                                                                                                                                                                                                                                                                                                                                               QVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSA-GVGAIFDRVLTELVS
                                                                                                                                                                                                                                                                                                                                                                                                   QLVLTLLEAEPPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \tt RKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKCLAMGMKREAVQEER-Q-R-GK-DRNENE-VESTSSAN---EDMP-VEKILEAELAVE
                                                                                                                                                                                                                                                           RFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKSG
                                                                                                                                                                                                                                                                                                                              QVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLAT-TS
                                                                                                                                                                                                                                                                                                                                                                                                                                    PKTETYVEANMG--L-N-PSSP-NDP--VTNICQAADKQLFTLVEWAKRIPHFSELPLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: ami
TOPOLOGY:
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ZIP: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116;
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                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO PCT/US91/00399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 514; DB 1;
Pred. No. 3.23e-35;
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                                                                                                                  PRT;
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28;

Gaps

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326 301 266 248

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368 322 308 262 248 208 188 157 128 99

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Sequence 4, Application PC/TUS9100399 GENERAL INFORMATION:

TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:

RETINOID METHODS

APPLICANT:

Mangelsdorf, Dr., Evans Dr., Ronald

David J.

CORRESPONDENCE ADDRESS:

ADDRESSEE:

STREET: 135 Sc CITY: Chicago

Illinois

USA

CURRENT APPLICATION DATA:

APPLICATION NUMBER: POFILING DATE: 19910122

PCT/US91/00399

CLASSIFICATION:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com

Floppy disk

60603

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/4FILING DATE: 09-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Mr., Steph

07/478,071

NAME: Reiter, Mr., S REGISTRATION NUMBER:

Mr., Stephen UMBER: 31192

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138 HICAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKRQRNRCQYCRY 197
                                                               ISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNA
                                                                                                                                                                                                                                                         PKTETYVEANMG--L-N-PSSP-NDP--VTNICQAADKQLFTLVEWAKRIPHFSELPLDD
                                                                                                                                                                                                                                                                                                     RKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPE
                                                                                                                                                                                                                                                                                                                                QKCLAMGMKREAVQEER-Q-R-GK-DRNENE-VESTSSAN----EDMP-VEKILEAELAVE
                                                                                                                                                                                                                                                                                                                                                              HFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRL
                                                                                                                                                     KMRDMQMDKTELGCLRAIVLFNPDSKGLSNPA-EVEA---L-R--EKVYASLE-AYCKHK 412
                                                                                                                                                                                 QVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLAT-TS
                                                                                                                                                                                                                                            QLVLTLLEAEPPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFD
                                                                                           YP-EQPG-RFAKLLLRLPALRSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEA 462
                                                                                                                        RFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKSG
                                                                                                                                                                                                              QVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSA-GVGAIFDRVLTELVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2: FITCH, EVEN, TABIN & FLANNERY 135 South LaSalle Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 3.23e 89; Mismatches
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Pred. No. 3.23e-35;
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      462
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                                                                                                                                                                                          133 HICAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKRQRNRCQYCRY 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: EVANS,
APPLICANT: MANGEL
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-546-9392 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: WO PCT FILING DATE: 22-JAN-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07, FILING DATE: 09-FEB-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                        TOPOLOGY: 1110---
MOLECULE TYPE: protein
MOLECULE TYPE: protein
MW; 1063517 CN;
TENCE 462 AA; 50811 MW; 1063517 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 08-NOV-199
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 21-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-AUG-1992 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                            QLVLTLLEAEPPHVLISRPSAPFTEASMMSLTKLADKELVHMISWAKKIPGFVELSLFD
                                                                                                                                                              QVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSA-GVGAIFDRVLIELVS
                                                                        PKTETYVEANMG--L-N-PSSP-NDP--VTNICQAADKQLFTLVEWAKRIPHFSELPLDD 296
                                                                                                       RKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPE 266
                                                                                                                                    QKCLAMGMKREAVQEER-Q-R-GK-DRNENE-VESTSSAN---EDMPVER-ILEAELAVE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & STREET: 444 SOUTH FLOWER STREET, SUITE 2000 CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: REITER, STEPHEN
                                                                                                                                                                                                                            116;
                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                     h 13.1%;
Similarity 33.0%;
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                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                              462 amino acids
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WENTION: RETINOID RECEPTOR COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-1994
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EM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                         Score 513; DB 1;
Pred. No. 3.98e-35;
89; Mismatches 119
                                                                                                                                                                                                                                                                                                                                                                            2
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                                                                                                                                                                                                                         Mismatches 119;
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                                                                                                                                                                                                                                                      Length 462
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                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                         28;
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                                            326
                355
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Matches Query Match

116;

Conservative

Local Similarity 33.0%;

13.2%;

SEQUENCE

MOLECULE TYPE:

ULE TYPE: protein 467 AA; 51216 MW; 1083042 CN;

TYPE: AMI

AMINO ACID

linear

TELEFAX: (619) 552-0095
TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 4:

TELEPHONE: (619) 552-1311

SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acid

467 amino acids

RESULT

US-08-336-408B-2

STANDARD;

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386 361 327 302 267 249 207 198 147

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                                                                                                               SEQUENCE
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  207
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                                                133 HICAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKRQRNRCQYCRY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application PC/TUS9100399 GENERAL INFORMATION:
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                                                                                                                                             TELEFAX: (619) 552-0095
TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/0039
FILING DATE: 19910122
                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/478,071
FILING DATE: 09-FEB-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                              TELEPHONE: (619) 552-1311
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: RETINOID RECEPTOR COMPOSITIONS AND TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mangelsdorf, Dr., APPLICANT: Evans Dr., Ronald
                  QKCLAMGMKREAVQEER-Q-R-GK-DRNENE-VESTSSAN----EDMPVER-ILEAELAVE 243
                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
 RKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPE
                                    HFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KMRDMQMDKTELGCLRAIVLFNPDSKGLSNPA-EVEA---L-R--EKVYASLE-AYCKHK 407
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                                                                                                                                                                                                                  NAME: Reiter, Mr., Stephen E. REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: 5085
                                                                                                                                TOPOLOGY: linear
                                                                                                                                        TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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FITCH, EVEN, TABIN & FLANNERY
                                                                                                              protein
50811 MW;
                                                                                 13.1%;
33.0%;
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                                                                       Score 513; DB 2; Le
Pred. No. 3.98e-35;
89; Mismatches 119;
                                                                                                               1063517 CN;
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266
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                                                                                                                                                         TELEPHONE: 619-546-19
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: EVANS, RONAL
APPLICANT: MANGELSDORF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
EILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: WO POST FILING DATE: 22-JAN-1991 PRIOR APPLICATION NUMBER: US OF APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 619-546-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                  NAME: REITER, STEPHEN E REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 9007
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COPOLOGY:
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444 SOUTH FLOWER STREET,
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LOWER STREET, SUITE 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO PCT/US91/00399
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                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00399
FILING DATE: 19910122
CLASSIFICATION DATA:
APPLICATION UMBER: 07/478,071
APPLICATION UMBER: 07/478,071
FILING DATE: 09-FEB-1990
                                                                                                                                                                                                                                                                                               Sequence 6, Application PC/TUS9100399
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mes 117; Conservative
                                                                                                                                                                                                                                          APPLICANT: Mangelsdorf, Dr., APPLICANT: Evans Dr., Ronald TITLE OF INVENTION: RETHODS
                  FILING DATE: 09-FEB-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                    COUNTRY:
                                                                                                                                                                              CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                    STREET:
REGISTRATION NUMBER:
                                                                                                                                                                                                             ADDRESSEE:
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          Reiter,
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         Mr., Stephen
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                                                                                                   Release #1.0, Version
                                                                                  PCT/US91/00399
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Pred. No. 1.11e-32;
94; Mismatches 120;
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Best Local :
                                         Matches
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Best Local Similarity 32.2%;
Matches 117; Conservative
                                                                                                                      APPLICANT: TAKAKU, FUMIMARO; ISHIKAWA, EVANS, RONALD M.; UMESONO, KAZUHIKO TITLE OF INVENTION: HUMAN GAMMA RETIN NUMBER OF SEQUENCES: 4 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/370,407 EILING DATE: 22-JUN-1989
                                                                                        SEQUENCE
                                                                                                                SEQ ID NO:
                                                                                                                                                                                                                  Patent No. 5260432
                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                    01-JAN-1900
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-1311
TELEFAX: (619) 552-095
TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
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90 CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNRCQVCRLQK 149
                                             Local
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MOLECULE TYPE: protein
JENCE 463 AA; 50978 MW; 1097932 CN;
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                                                                                       LENGTH: 454
CE 492 AA;
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larity 28.4%;
Conservative
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                                                                                        54527 MW; 1333563 CN;
                                                                                                                                                                                                   FUMIMARO; ISHIKAWA,
                                    Score 441; DB 3;
Pred. No. 1.27e-28;
88; Mismatches 140
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Pred. No. 1.11e-32,
94; Mismatches 120
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                                       140;
                                                                                                                                                                             ACID RECEPTOR
                                                             Length 454;
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Best Local S
Matches 9
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TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
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                                                                                                                                                                                                                                                                                                                                                                                    11.2%;
Local Similarity 26.9%;
les 94; Conservation
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                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                           LPLEMDDTE----TG--LL-SAICLICGDRQDLEEPTKVDKLQBPLLEALK-IYIRKRRP
                                                                                                                                                                                                                                                                                                                                 CAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRK 208
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                                                                    RELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKSGIS
                                                                                                                                   RLL-ESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSRF
                                                                                                                                                                TLLKAAC-LDILILRICTRYTPEQDTMTFSDGLTLNRTQ-MHNAGFGPLTDLVFTFANQL
                                                                                                                                                                                                VLTLLEAEPPHVLISRPSAPFTEASMMSLTKLADKELVHMISWAKKIPGFVELSLFDQV
                                                                                                                                                                                                                                                                 CYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQL
                                  SKPH-M-FPKILMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMME
   SQQQSMRLANLLMLLSHYRHASNKGMEHLLNMKCKNVVPVYDLLLEMLN
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CE 398 AA; 44842 MW; 907111 CN;
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Pred. No. 1.91e-28;
97; Mismatches 136;
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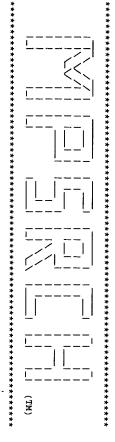
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Best Local Similarity 26.9%;
Matches 94; Conservative
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FILING DATE: 17-DEC-1987
PRIOR APPLICATION DATA:
SEQ ID NO:2:
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APPLICANT: BLAUDIN DE THE, HUGHES; MARCHIO, PIERRE; DEJEAN, ANNE
TITLE OF INVENTION: STEROID/THYROID HORMONE PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPAT
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                                                                                                                                                                                                                                                                                                              81 CFYCQDKSSGYHYGYSACEGCKGFFRRSIQKNMIYTCHRDKNCYINKYTRNRCQYCRLQK 140
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CURRENT APPLICATION DATA:
                                                                                                                                              TLLKAAC-LDILILRICTRYTPEQDTMTFSDGLTLNRTQ-MHNAGFGPLTDLVFTFANQL 309
                                                                                                                                                                            VLTLLEAEPPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFDQV
                              SKPH-M-EPKILMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMME
                                                                         LPLEMDDTE----TG--LL-SAICLICGDRQDLEEPTKVDKLQEPLLEALK-IYIRKRRP 361
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Pred. No. 1.91e-28;
97; Mismatches 136;
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MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Tue Nov 3 04:15:30 1998; MasPar time 2128.26 Seconds 1215.488 Million cell updates/sec

Tabular output not generated.

Title: >US-08-906-365-1

Description:
Perfect Score:
N.A. Sequence: 1686 (1-1686) from US08906365.seq

Sequence: Comp: 1 cagccattatacttgcccac......agaacccacagtctcagtga 1686 gtcggtaatatgaacgggtg......tcttgggtgtcagagtcact

Scoring table: TABLE default Gap 6

Nmatch STD Dbase 0; Query 0

Searched: 1988617 seqs, 767163441 bases × 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: 1:em_est10 2:em_est11 genbank-est107 embl-est55

Database:

3:gb_est1 4:gb_est10 5:gb_est11 6:gb_est12 7:gb_est13 8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est17 11:gb_est18 13:gb_est2 15:gb_est21 11:gb_est21 17:gb_est21 17:gb_est21 17:gb_est21 17:gb_est22 18:gb_est23 19:gb_est24 20:gb_est3 21:gb_est4 22:gb_est5 23:gb_est6 24:gb_est7 25:gb_est8 26:gb_est9 27:gb_gss

Mean 11.528; Variance 1.960; scale 5.882

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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462 280												% Query Match Length DB
16 16	21	21	10	13	16	16	7	13	13	13	15	BG
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zv26g03.rl Soares NhHM nx21b07.sl NCI_CGAP_GC	ys69hll.rl Homo sapien	ys81d07.rl Homo sapien	ma83b04.rl Soares mous	97SN1784 Rice Immature	EST194087 Normalized r	EST197421 Normalized r	vh95el0.rl Barstead mo	97SN1787 Rice Immature	97SN1787 Rice Immature	ny79f02.sl NCI_CGAP_GC	zr14e02.rl Stratagene	Description
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ydsball.rl Homo Sapien zj49d12.sl Soares feta C.elegans cDNA clone y zk54a08.rl Soares preg me32d01.rl Soares mous ud60g08.yl Sugano mous Homo sapiens ntcon2 co	.rl Soares t .rl Soares t .rl Soares t ns cDNA clon 3 Infant bra 1 HSC172 cel .rl Stratage piens ntcon2	seq.F Fetal .rl Homo sa .rl Soares ! Activated !lo Normaliz .rl Soares .rl Soares .rl Soares .rl Soares	md56a06.rl Stratagene md56a06.rl Soares mous mg80b08.rl Soares mous ov45e08.rl Soarestest 97SN1784 Rice Immature GM14739.5prime GM Dros oj33h03.sl NCI_CGAP_Lu md45d07.rl Soares mous mh80b06.rl Soares mous
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ALIGNMENTS

en Trock	FEATURES		COMMENT	TITLE	REFERENCE	NID KEYWORDS SOURCE ORGANISM	RESULT 1 LOCUS DEFINITION ACCESSION
/organism="Homo sapiens" /organism="Homo sapiens" /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: /hol; Cloned unidirectionally. Primer: Oligo dT. Differentiated, post mitotic hNT neurons. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'	Insert Length: 1309 Std Error: 0.00 Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 357. Location/Qualifiers	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fal: 314 286 1810 Fax: 314 286 1810 Email: estewatson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	Contact: Wilson RK Washington University School of Medicine	Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project Unpublished (1997)	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 531) Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,	g1844690 EST. human. Homo sapiens	AA224131 531 bp mRNA EST 11-MAR-1998 zr14e02.rl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 648794 5', mRNA sequence.

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA744644 466 bp mRNA EST 07-FEB-1998 ny79f02.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1284507 similar to gb:M12674 ESTROGEN RECEPTOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                    High
                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
Ph.D., Gerald Marti, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA744644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; Metazoa; Chordata; Vertebrata; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                          CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: M. Bento Soares, Ph.D., Sonaldo, Ph.D.
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CTCGAGTTTTTTTTTTTTTTT 3'"
/db_xref="CDB:5589314"
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/clone="648794"
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/lab_host="SOLR (kanamycin resistant)"
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Query Match 4.0%;
Best Local Similarity 11.8%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
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Best Local Similarity 82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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EST.
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97SN1787 Rice Immature Seed Lambda
cDNA clone 97SN1787, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: myeun@sun20.asti.re.kr
Submitted by Back Hie Nahm, Dept of
University, Yongin, Korea. 449-728 b
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Cytogenetics
National Inst. of Agri. Sci. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 252)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R,
NAhm,M.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., 1
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA754459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Eun M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Large-scale
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Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poaceae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/Cultivar="Milyang23"
/Cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="Vector: Directional cDNA library inserted into lambda ZAPI
XhoI; Directional cDNA library inserted into lambda ZAPI
vector at 5'end with EcoRI and 3' end with Xho I site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library
                                                                                                                                                                 /dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 ot
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4530"
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                                                                                                                                                                                                                                                                                                          /clone_lib="Rice Immature Seed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Score 68; DB 13;
Pred. No. 4.00e-88,
123; Mismatches 7!
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2.42e-105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            f Biological Science, Myongji
bhnahm@bioserver.myongji.ac.kr
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Best Local Similarity 14.2%;
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                 VNWBNVSGDWHYWBVBNTKVDVGNHTRCSRWRBVTRM-AHYHDYTNCBBYNNNDYHMWHB 126
                                                 cgccccatgtgctgatcagccgcccagtgcgcccttcaccgaggcctccatgatgatgt 982
                                                                        VRGCCCCBAWMITSYBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWS-TMTWGT 67
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EST.
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Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yougin, Korea. 449-728 bhnahm@bioserver.myongji.ac.
Seq primer: M13 Reverse Primer.
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National Inst. of Agri. Sci. and
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
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Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., F
Lee,M.C. and Eun,M.Y.
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                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: xhoI; Directional cDNA library inserted into lambda ZAPII vector at 5 end with EcoRI and 3' end with Xho I site." /db_xref="taxon:4530" /clone="97SN1787"
                                                                                                                                                                                                                  /dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 ot
                                                                                                                                                                                                                                                                            /tissue_type="Immature Seed"
                                                                                                                                                                                                                                                                                           /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="Milyang23"
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
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Pred. No. 1.46e-77
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WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 534)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA517920 534 bp mRNA EST vh95e10.rl Barstead mouse myotubes MPLRB5 Mus 902058 5' similar to gb:M34476 Mouse retinoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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Vertebrata; Mammalia;
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Location/Qualifiers
3.6%;
llarity 66.7%;
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                                                                                                                                                                                     Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins."

/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                               3'); double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector.
                                                                                                                                                    /clone_lib="Barstead
/cell_line="C2C12"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C3H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                  'lab_host="DH10B"
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                                                                                                                                  ATCAATGATGCAATCGTTTCTTCCAGCACAAAGGTAATTGTGCTGTCCTTCCACTGCTCT 134
                                                                                                                                                                          cattoccacttogtaacacttocgaagtoggoaggootggoagctottgogooggttttt
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                                                         tttaaaaaaggccttacatccttcacacgaccagactccatagtgatatcccgatgcgta
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1 (chases 1 to 384)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quacken Kerlavage, A.R. and Adams, M.D.
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clone RPLAC64 3' end,
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primer: M13-21.
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larity 64.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus sp."
/note="Organ: placenta; Vector:
Site_2: NotI"
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/clone="RPLAC64"
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Pred. No. 4.37e-63;
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9712, Medical Center Drive, R
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
         rice.
Oryza sativa
Cukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; L
                                                                     AA754458 247 bp mRNA E
97SN1784 Rice Immature Seed Lambda ZAPII
cDNA clone 97SN1784, mRNA sequence.
AA754458
g2801164
EST.
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128; Conser
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EST194087 Normalized
clone RPLAF19 3' end,
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1 (bases 1 to 384)

Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J

Kerlavage,A.R. and Adams,M.D.
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Rodentia; Sciurognathi; Muridae; Murinae;
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Site_2: Noti"
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/db_xref="taxon:10118"
/clone="RPLAF19"
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/note="Organ: placenta; Vector: pT7T3Pac;
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Oryza
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Pred. No. 4.37e-63;
0; Mismatches 72;
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similar to
sequence.
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Large = craic --
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Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 390) Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, M., Beisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morr
                                                                                          Mus musculus
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National Inst. of Agri. Sci.
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                                                                                                              house mouse
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Similarity 14.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPI
vector at 5'end with EcoRI and 3' end with Xho I site."
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/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
16 c 21 g 34 t 169 ot)
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/clone="97SN1784"
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b gb:L13740 EAR
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                    Dietrich, N.,
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H91890 403 bp mRNA EST ys81d07.rl Homo sapiens cDNA clone 221197 5 gb:X51417_cds1 STEROID HORMONE RECEPTOR ERR
                                                                                                                                                                                                                                                                                                                                                                                                                                128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free
IMAGE Consortium (info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel:
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Similarity 62.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH1OB (ampicillin resistant)"
106 c 114 g 100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dr. Minoru Ko (Wayne State University)."
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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5.21e-55;
5.7 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through LLNL ; v) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 390;
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similar to
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Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. )
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 403)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian male and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and
                                                                                                                                                                                                                                           ys69h11.rl Homo sapiens
gb:X51417_cds1 STEROID H
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This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1995)
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Similarity 66.7%;
104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.Fatima Bonaldo.
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/clone="221197"
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Pred. No. 5.21e-55;
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similar to
                                                            Eukaryotae;
Vertebrata;
                                                                                                      Homo sapiens
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Source: IMAGE Consortium,
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larity 65.7%;
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/clone="220101"
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  Allen,M.,
                                                            mitochondrial eukaryotes; Metazoa; Chordata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Bowles, L.,
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Jost,S.,
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                                                                                                                                                                                                                                                                                                                CTGTCAATACTGCAGGTTACAGAGATGTATTGCGTTTGGAATG 452
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                                              g2984958
EST.
                                                                                                         AA876157 280 bp mkNA 21007.51 NCI_CGAP_GC3 HOMO Sapiens cDNA clone IMAGE:1256725 3' similar to gb:M11050 GLUCOCORTICOID RECEPTOR, BETA (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 334.
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4444 Forest Park Parkway, Box 8501, St. 1
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AA876157
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Fax: 314 286 1810
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/note="Organ: mixed (see below); Vector: pT773D-Pac
/note="Organ: mixed (see below); Vector: pT773D-Pac
/(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_1: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260332-265223,
340488-345479, and 484488-489479."
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99 c 94 g
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/clone="754804"
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61.9%;
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Pred. No. 5.16e-57;
0; Mismatches 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106;
                                                                                                                                                                                                                         (HUMAN);, mRNA sequence.
AA157597
g1729205
                                                                                                                                                                                                                                                                                                                  AALD/59/ 412 bp mRNA EST 2044a02.rl Stratagene endothelial cell 937223 clone 589706 5' similar to gb:X07282 RETINOIC
Vertebrata; Eutheria; Primates;
1 (bases 1 to 412)
Hillier,L., Clark,N., Dubuque,T.
                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
                                                                                                                                 human.
Homo sapiens
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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//Organism="Momo sa
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/clone_lib="NCI_CGAP_GC3"
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Pred. No. 4.93e-51;
0; Mismatches 56
Dubuque, T.,
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Elliston, K.,
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RECEPTOR BETA-2
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4444 Forest Park Parkway, Box 8501,
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                                                                                     1 (bases 1 to 508)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W53545 508 bp mRNA EST 03-JUN-1996 md56a06.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 372370 5' similar to gb:X57528 M.musculus mRNA for retinc
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
WashU-Merck EST Project
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Vertebrata; Eutheria; Rodentia; Sciurognathi; N
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                                  The WashU-HHMI Mouse EST Project
                                                                    Waterston, R.
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d. No. 5.13e-53;
Mismatches 60;
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                                                                          accggcgcaagagctgccaggcctgccgacttcggaagtgttacgaagtgggaatg
                                                                                                           TGACCCGGAACCGCTGCCAGTACTGCCGGCTGCAGAAATGTTTCGACGTGGGCATG 408
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    Location/Qualifiers
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Fax: 314 286 1810
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Washington University School of Medicinep
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: mob.REGA+ET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
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Similarity 63.6%;
112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.7], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ. from 2]; double-stranded cDNA was ligated t Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

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rch completed: Tue time : 2152 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Nov 2 16:24:20 1998; MasPar time 20.72 Seconds 413.984 Million cell updates/sec

Tabular output not generated

Title: >US-08-906-365-2 (1-530) from US08906365.pep

Description: Perfect Score: 3904 1 MD:

MDIKNSPSSLNSPSSYNCSQ.....ECSPAEDSKSKEGSQNPQSQ 530

Scoring table: PAM 150 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part2 72:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 36.033; Variance 154.129; scale 0.234

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	3904	100.0	530	28	W33215	Human oestrogen recep	0.00e+00
2	3582	91.8	485	21	W14724	oestrogen	0.00e+00
ω	3532	90.5	477	28	W33212	oestrogen	0.00e+00
4	3274	83.9	485	21	W14723	estrogen r	0.00e+00
տ	3250	83.2	485	21	W14725	Mouse oestrogen recep	0.00e+00
o	3099	79.4		27	W33213		4.32e-293
7	3099	79.4	418	28	W33214		4.32e-293
œ	1714	43.9	233	27	W33211		2.24e-154
·	1671	42.8	595	N	P70543	Human oestrogen recep	4.30e-150
10	1424	36.5	334	N	P80925		1.58e-125
11	807	20.7	433	N	P80931	huma	1.04e-64
12	800	20.5	521	N	P80930	of human	5.02e-64
13	614	15.7	777	N	P80919		5.47e-46
14	614	15.7	777	28	W44700	Mutant nuclear glucoc	5.47e-46
15	590	15.1	1070	23	W17789	Green fluorescent pro	1.11e-43
16	576	14.8	902	ω	R12224	Rat androgen receptor	2.46e-42
17	570	14.6	902	_	P93110	Rat androgen receptor	9.28e-42
18	570	14.6	902	μ	P91006		9.28e-42

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noid X	(D	specific murine	$^{\circ}$	nce of nuclear	retino	Mouse RXR-gamma retin	gamma.	RXR-alpha re	Mouse RXR-alpha retin		Sequence of the human	mRXR-beta.	hRXR-beta2.		H2RIIBP nuclear hormo	Human H-2RIIBP.	hRXR-beta1.	trog	n oestroge	cept	en re	₽.	recep	Human androgen recept	ᠬ	ndian androden recebe
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ALIGNMENTS

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Query Match Best Local Similarity 100.0%; Matches 530; Conservative	W33215 standard; Protein; 5 20 APR-1998 (first entry) Human oestrogen receptor prosetin; estone; estroil; screening. EP-798378-A2. 01-OCT#1997; 200903. 25-MAR-1996; EP-203284. 26-MAR-1996; EP-203284. 26-MAR-1996; EP-200820. (ALKU) AKZO NOBEL NV. Dijkema R, Mosselman S; WPI, 97-473189/44. N-PSDB; T88415. N-PSDB; T8841
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Pro	W33215 standard; Protein; 530 AA. W33215; W33215; W33215; Human oestrogen receptor protein #2. Oestrogen receptor protein; steroid; estone; estriol; screening. Homo sapiens. EEP-798378-A2. 01-OCT#1997; 200903. 25-MAR-1996; EP-200820. (ALKU) AKZO NOBEL NV. Dijkema R, Mosselman S; WPI; 97-473188/44. N-PSDB; T88415. N-PSDB; T88415. N-PSDB; T88415. DNA encoding estrogen receptor - use identify novel ligands or hormonal a claim 4; Page 35-37; 45pp; English. This sequence represents a novel oes human testis cDNA in order to study codons using 5' RACE-PCR technology. De activated by estradiol, estone an assay for the identification of new sequence 530 AA;
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Gaps	W33215 standard; Protein; 530 AA. W33215 standard; Protein; 530 AA; Extract of the identification of new drugs e.g. novel ligands or hormonal analogues. Sequence 530 AA;
0;	W33215 standard; Protein; 530 AA. W33215; W33215; 20 APR-1998 (first entry) Human oestrogen receptor protein #2. Oestrogen receptor protein; steroid; alternative splicing; estradiol; estone; estriol; screening. Homo sapiens. EP-798378-A2. 01-OCT#1997; 200903. 22-NOV-1996; EP-2003204. 26-NAR-1997; EP-200820. (ALKU) AKZO NOBEL NV. Dijkema R, Mosselman S; WPI; 97-473188/44. N-PSDB; T88415. N-PSDB; T88415. DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues Claim 4; Page 35-37; 45pp; English. This sequence represents a novel oestrogen binding protein isolated from human testis cDNA in order to study upstream translation-initiation codons using 5' RACE-PCR technology. This receptor is able to bind and be activated by estradiol, estone and estriol, can be used in a screening assay for the identification of new drugs e.g. novel ligands or hormonal analogues. Sequence 530 AA;
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08-SEP-1995; GB-018272.
15-MAR-1996; GB-005550.
11-APR-1996; GB-007532.
08-MAY-1996; GB-009576.
(KARO-) KARO BIO AB.
                                                                                                                                                                                                                                                                                      13-MAR-1997.
09-SEP-1996;
08-SEP-1995;
15-MAR-1996;
11-APR-1996;
08-MAY-1996;
                                                        A novel human orphan receptor (W14724) is related to the known oestrogen receptor ER-alpha, and has been designated ER-beta. It is an oestrogen receptor-related nuclear receptor. The ER-beta amino acid sequence was deduced from a cDNA clone (T62843) isolated from a human testis cDNA library. Rat, human and mouse ER-beta (W14723-25) can be used to isolate molecules for use in the treatment of cardiovascular diseases, central nervous system diseases, osteoporosis, prostate or ovarian cancer or benign prostatic hyperplasia and to test environmental chemicals for cestrogenic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human oestrogen receptor beta (ER-beta).
Orphan receptor; oestrogen receptor beta; ER-beta;
Outhan receptor; prostate cancer; benign prostatic
nuclear receptor; prostate cancer; benign prostatic
ovary cancer; cardiovascular disease; osteoporosis;
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W14724;
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25-MAR-1997; 2
22-NOV-1996; E
26-MAR-1996; E
(ALKU ) AKZO N
                                                                                                                                                                       N-PSDB; T88412.

NA encoding estrogen receptor - useful in screening assay to lidentify novel ligands or hormonal analogues claim 4; Page 18-20; 45pp; English.

This sequence represents a novel oestrogen binding protein. The cDI sequence which encodes this protein can be alternatively spliced resulting in the detection of additional transcripts (see T88413). This receptor is able to bind and be activated by estradiol, estone estriol, can be used in a screening assay for the identification of drugs e.g. novel ligands or hormonal analogues.

Sequence 477 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                          13-MAR-1997.
09-SEP-1996;
08-SEP-1995;
15-MAR-1996;
11-APR-1996;
08-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-1997
Rat oestroge
Orphan recep
                                                      Claim 1; Fig 1; 45pp; English.

A novel rat orphan receptor (W14723) is related to the known oestrogen receptor ER-alpha, and has beeignated ER-beta. It is an oestrogen receptor related nuclear receptor. The ER-be amino acid sequence was deduced from a cDNA clone (T62842) isolate from a rat prostate cDNA library. Rat, human and mouse ER-beta (W14723-25) can be used to isolate molecules for use in the treatment of cardiovascular diseases, central nervous system diseases, osteoporosis, prostate or ovarian cancer or benign prostatic hyperplasia and to test environmental chemicals for
                                                                                                                                                                                       New isolated
treating e.g.
                                                                                                                                                                                                              N-PSDB; T62842.
                                                                                                                                                                                                                     (KARO-) KARO BIO AB.
Enmark E, Gustafsson
WPI; 97-192842/17.
                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                                                                                 environment;
                                                                                                                                                                                                                                                                                                                                                                                                                           ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                      nuclear receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W14723
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W14723 standard;
                                               oestrogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                           cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                         strogen receptor beta (ER-beta).
receptor; oestrogen receptor beta; ER-beta;
r receptor; prostate cancer; benign prostatic
cancer; cardiovascular disease; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                      ds
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                                    485
                                                                                                                                                                                                                                                       ; E03933.
; GB-018272.
; GB-005550.
; GB-007532.
; GB-009576.
                                            activity.
                                                                                                                                                                                                 oestrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                       cancers,
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
104.169
/label= DNA-binding_
259..457
/label= Ligand-bindi
                                    Ą,
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 . 9%;
                                                                                                                                                                                     receptor beta - used to develop CNS diseases, osteoporosis or ca
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                                                                                                                                                                                                                                                                                                                                                               DNA-binding_domain
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Pred.
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3274;
No. 0.
 DB 21;
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         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                     hyperplasia;
                                                                                                                                                                                       cardiovascular
                                                                                                                                                                                                 prods.
            485;
                                                                                                                 isolated
                                                                                                                          ER-beta
                                                                                                                                                                                                  for
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                                                                                                                                                                                                                             09-SEP-1996; E03933.

08-SEP-1995; GB-018272.

15-MAR-1996; GB-005550.

11-APR-1996; GB-007532.

08-MAY-1996; GB-009576.

(KARO-) KARO BIO AB.
A novel mouse orphan receptor (W14725) is related to oestrogen receptor ER-alpha, and has been designated It is an oestrogen receptor related nuclear receptor amino acid sequence was deduced from a cDNA clone (T0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse oestrogen receptor beta; Ex-uern,
Orphan receptor; oestrogen receptor beta; Ex-uern,
Orphan receptor; prostate cancer; benign prostatic
cancer; benign prostatic cancer; benign prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W14725;
W14725;
                                                                                                                                             Enmark E, Gustafsson J
WPI; 97-192842/17.
N-PSDB; T62844.
New isolated oestrogen
                                                                                      Claim
                                                                                                        disease
                                                                                                                                                                                                                                                                                                                                                               WO9709348-A2.
13-MAR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                              domain
                                                                                                                           treating
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                                                                                      1; Fig
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                                                                                      14A;
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gen receptor beta (ER-beta).
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                                                                                                                             cancers,
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
104..169
/label= DNA-binding_domain
260..457
/label= Ligand-binding_domai
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                                                            45pp; Englis
han receptor
                                                                                                                                                                                                                'n
                                                                                                                         receptor beta CNS diseases,
                                                                                  English
                                                                                                                                                                                                                                                                                                                                                                                                      Ligand-binding_domain
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    used to develop prods. for osteoporosis or cardiovascular

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                   ER-beta.
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                                                              the known
                       ER-beta
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EP-798378-A2.
01-OCT-1997.
25-MAR-1997; 200903.
22-NOV-1996; EP-203284.
26-MAR-1996; EP-200820.
(ALKU) AKZO NOBEL NV.
Dijkema R, Mosselman S;
WPI; 97-473188/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           central nervous system diseases, osteoporosis, prostate or ovari cancer or benign prostatic hyperplasia and to test environmental chemicals for ostrogenic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecules for use
                                                  DNA encoding estrogen receptor - us identify novel ligands or hormonal Claim 4; page 20-22; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
         This partial sequence represents a splice variant of a novel cestribinding protein, detected by screening a human testis cDNA library. This protein contains an alternative exon 8 (exon 8B) of the novel cestrogen receptor represented. As a consequence of the introduction
                                                                                                                                                                                                     Oestrogen
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the treatment of cardiovascular diseases,
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22-NOV-1996; EP-203284.
26-MAR-1996; EP-200820.
(ALKU ) AKZO NOBEL NV.
Dijkema R, MOSSelman S;
WPI; 97-473188/44.
                                         DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues (laim 4; Page 30-32; 45pp; English.
This sequence represents a splice variant of a novel oestrogen binding protein isolated from human thymus tissue. This protein contains an alternative exon 8 (exon 8C) of the novel oestrogen receptor represented in T88412. This novel receptor is able to bind and be activated by estradiol, estone and estriol, can be used in a screening assay for the identification of new drugs e.g. novel ligands or hormonal analogues. This variant does not contain an AF-2 region and therefore probably lacks the ability to modulate transcription of target genes in a ligand dependent faction.
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01-OCT-1997.
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22-NOV-1996; EP-203284.
26-MAR-1996; EP-200820.
(ALKU ) AKZO NOBEL NV.
Dijkema R. Mosselman S;
WPI; 97-473188/44.
N-PSDB; T88412.
                                                                                                                                                                                                                                                                                                                   DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues Claim 4: Page 16-17; 45pp; English.

This sequence encodes the ligand binding domain of a novel constrogen binding protein, detected by screening a human testis cDNA library. This receptor is able to bind and be activated by estradiol, estone and estriol, can be used in a screening assay identification of new drugs e.g. novel ligands or hormonal
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Solutions of the protein protein an expression system from cDNA operably inked to control sequences compatible with eukaryotic host cells.

This method allows expression under conditions which favour appropriate post-translational processing. It also produces large amts. of purified protein useful in the design of agonist and antagonist cpds. for study of the mechanism of action of the steroid binding proteins in general, and for use in diagnostic assays for the proteins or antibodies to them. These assays are important in, eg the diagnosis of tumour sensitivities to steroid metabolism. Suitable host cells are VERO, Sequence 595 AA;
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27-AUG-1987.
18-FEB-1987; U00341.
20-FEB-1986; US-833829.
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23-OCT-1987; U02782.
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(SALK) Salk Inst for Bio
Evans RM, Weinberger CA,
WPI; 88-133242/19.
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DNAs encoding hormone receptors and the hormone receptors themselves are claimed. The DNA can be used to make the hormone receptor proteins and functional modified forms in quantities not previously possible. The receptor proteins can be used to screen cpds. for receptor-argonist or receptor-antagonist activity. They can also be used in diagnostic assays. Also claimed is pure DNA encoding oestrogen related receptors will provide here? and here? and here?
                                                                                                          comprising glucocorticoid, mineralocorticoid, thyroid hormone and novel hormone receptors
and novel hormone receptors
Claim 17; Fig V-1(B)-1 and -2; 243pp; English.

DNAs encoding hormone receptors and the hormone receptor proteins an functional modified forms in quantities not previously possible. The functional modified forms in quantities not previously possible. The receptor proteins can be used to screen opds. for receptor-agonist or receptor-antagonist activity. They can also be used in diagnostic ass also claimed is pure DNA encoding oestrogen-related receptors hERRI and hERR2 and hERRI and hERR2. The new hERRI and hERR2 receptors will properly the province of the provin
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant DNA encoding hormone recpetors - comprising glucocorticoid, mineralocorticoid,
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521 AA;
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Best Local Similarity
Matches 97; Conser
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Claim 24; Fig I-2(1) to (2); 243pp; English.

DNAs encoding hormone receptors and the hormone receptors themselves are claimed. The DNA can be used to make the hormone receptor proteins and functional modified forms in quantities not previously possible. The receptor proteins can be used to screen cpds. for receptor-agonist or receptor-antagonist activity. They can also be used in diagnostic assays. Sequence 777 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant DNA encoding hose comprising glucocorticoid, read and novel hormone receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormone recpetors - d, mineralocorticoid, thyroid hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 614; DB 2;
Pred. No. 5.47e-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 5.02e-64; 74; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Contains is the amino acid sequence of in the region encoding the ligand correceptor (NGR), especially mutated in the region encoding the ligand content of the composition (LBD), such that the activity of the receptor is induced concerned by a synthetic glucocorticoid ligand than by a natural collection of transition mutation is a point mutation in the coding concerned at transition mutation) generated by site-directed mutagenesis. This causes a replacement of the lie region between helices in and 12. This causes a replacement of the region between helices in and 12. The mutant coding sequence is used to generate a fusion protein comprising a protein whose activity is to be regulated by and fused to the NGR sequence. The protein is preferably a recombinase, especially the cre recombinase from bacteriophage P1 (see V05702). The sequence containing the fusion protein, and vectors containing it, are used to treat colls either ex vivo or in vitro for use in gene therapy. Vectors containing and expressing the protein allow the transfer of heterologous genes to the cells' genome by recombinase-directed recombination at loxp sites. By using a mutated LBD, normal physiological levels of the ligand of the induce recombinated LBD, normal physiological levels of the ligand can be combinated.
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Brocard JB, Chambon PH,
Nicolas JC, Roux S;
WPI; 97-451186/42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W44700 standard;
W44700;
12-MAY-1998 (fil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; V05701.
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301
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TLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHND 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not induce recombination. This requires an
                                                                                                                                            ylcagrndciidkirrkncpacryrkclqagmnl-earktk-k-kikgiqqattg-v-sq
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                                                lggrqviaavkwakaipgfrnlhlddqmtllqyswmflmafalgwrsyrqssanllcfap
                                                                                                             GKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRPSAPFTEAS--MMMSLTK
                                                                                                                                                                                                                           YICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCA
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97; Conser
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Pred.
84; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614; DB 28;
No. 5.47e-46;
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                                                                                                                                                                                                                                                                                                                                                                         Manmalian cell having a plurality of steroid receptor response elements - can be directly detected when bound by fluorescently related steroid receptor labelied steroid receptor SC Claim 9; Page 67-72; 100pp; English.

A fusion protein (W17789) comprises jellyfish green fluorescent protein (GFP) fused to rat glucocorticoid receptor (GR) via a Glycortein (GFP) fused to rat glucocorticoid receptor (GR) via a Glycortein (GFP) fused to rat glucocorticoid receptor (GR) via a Glycortein and cortein and the GFP moiety contains an S65T substn. and the GFP moiety contains and S7T substn. and the GFP moiety contains and ATCC CRI-11988). Contg. a number of steroid receptor response elements in array, is used to visualise directly the interaction of GR and its binding site in chromatin using the fluorescently-labelled GR. This provides the direct opportunity to visualise receptor/target interactions and can be used to screen for ligands that activate gene targetting or translocation of steroid receptors in the nucleus of a mammalian cell.
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Green fluorescent protein-glucocorticoid receptor fusion. Green fluorescent protein; GFP; glucocorticoid receptor; steroid receptor; transcription factor; DNA binding molecule. Chimaeric Aequoria victoria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 15
W17789 standard; Protein; 1070 AA.
W17789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUN-1997.
06-DEC-1996; U19516.
08-DEC-1995; US-008373.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Hager GL, Htun H;
WPI; 97-319778/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain
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ASPVTGPGSK-RDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCT 192
                                                                                                                                                                                                                                                                  -ivpaalpq-ltpt-lv-slleviepevlyagydssvpdsawrimttlnmlggrqviaav 868
                                                                                                                                                                                                           idkirrkncpacryrkclqagmn1-earktk-k-kikgiqqatag-v-sqdtsenpn-kt 812
                                                             SWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHP-GKLI-FAPDLVLDRDEGK
                                                                                                                           PRVRELLLDALSPEQLYLTLLEAEPPHVLISRPSAPFTEAS - - MMMSLTKLADKELVHMI
                                                                                                                                                                                         IDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHA 252
                                                                                                                                                                                                                                                                                                              15.1%;
Similarity 33.2%;
93; Conservation
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/label= Linker
271..1070
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261...270
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                                                                                                                                                                                                                                                                                                              Score 590; DB 23; Length 1070; Pred. No. 1.11e-43; 83; Mismatches 88; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein"
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